					0:1	TTTD	Trrp Intronic
O Mann	Coriell DNA Panel(s)	Amplicon No. Total SNPs Missense Sticin	I otal SNFS	MISSEUSE	SHCH	CITY	ATTENDED
Gene Iname		Ç					
				,	•	t	7
	4. C1 . 10 4 2 2 7 1 2 2 4	74	9	0	7	_	17
A minonentidase P (XPNPEP2)	74 + 47 (33AA) +14ht	ţ	3	. ,	ı	•	_
Criminopolitical Company of Committee	100 CATO CATO 1734	7	14	7	n	7	4
Readykinin B1 recentor (BDKRB1)	24+ 95 (8AA, 105 CAU) +12pt	•	•		•	1.4	-
Country Country Country Country	10 / A A A A A A A A A A A A A A A A A A	12	36	m	.7	14	/ 1
(Bradvkinin B2 receptor (BDKKB2)	74 (8AA) +12pt	1		4	,	c	c
	ta01 : 14 40 40	7	6	-	•	c	c
NK1 tachykinin receptor (TACK1)	74 (OAA) +14pt	. ;	. `	•	c	<	0
CIMIN)	24 (8 A A) +12nt	10	0	7	4	>	1
CI esterase innibitor (CINE)	24 (2777) 17Eb	ι	4	-	_	c	2
V. 1135-25 1 (VI VI)	7 (7AA) +12pt	ი	0	-	4	1	1 1
Namikiem 1 (new)	- J : (~ : )	c	5	_	٠,		
Drotages Inhihitor 4 (PI4)	7 (7AA) +12pt	0	71	-	٠ د	٠ (	
LIUMAN TIMITUM T (LA.)		ć	o	_	_	=	~
Angiotensin Converting Enzyme 2 (ACE2) 7 (7AA) +12pt	(JE2) 7 (JAA) +12pt	077			,		
			122	0	2	30	65
Totale.			771	`	2	1	

Totals:

oca cua	CDWA SEQ POS	SACE																							926	8												awa.	2000		200	3604	3696	3456	3866				672				1639				1278	22,	98	88	288		897				35	462	22.2	705		\$					833	1061	1668
0.00	CDNA SEG ID	UBO/24.1													-						1				NM 0007101	NM 000710.1												ALL COMMON !	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20000	NM 000623.1	NM 000623 1	NM_0006231	NM 000623.1	NM 0006231			NA notice 2	NM 001068.2			NM_001058.2	NM 001058.2	NM 0010682			NM 000062.1	NM 000062.1	NM 000062.1	NM 000062.1	NM 0022571		NM 002267.1				W 000710	NM 000710.1	MM 0007101	NA 000710.1		WH 000623					MM 000623.1	NM 0006231	MM 000823.1
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		di dagcarara	TOCOCOANO	200000000000000000000000000000000000000	AL CONTOUR OF	MAIN AGGGTGGCC	MACCOTT	I GTTTCAGA	a) THEOTOGE	TOARTCACC	CTCCACCA	CAAGOOF	200000	10000000	131	GGCTCGAGC	<b>GCTGATCTG</b>	GACATA	ставсттт	GGGAGGAG	GAGAGGCTG	COCAGGAAC	Tagacccc	TOTITICACE	N GCTCTTCA	BOCARCACT	GATAAGAAA	ACCCIOTOT	GCCTATAAT	COULD DO S	GCGGCGCC	CCGCGCCCA	тооссотет	CTGGGGTGC	TOGGGACAG	CAGCACAGT	COCOCTON	morron	200000	TOGGTGGGT	Tagorocot	CACAGGACA	ACAGATGT	aracreraa	CATTCCT	TTGCCTAG	AACCTGGGG	CCCATCACC	MATGACACAG	осстаст	TITCI TTGGGAAAA	ACAGCATGA	AGTGTGAGG	aAgggTgTg	AGGGAAT	TGCATCTCT	CAGGATATG	TOAACCCAT	AATGAAGAA	тастстава	acacrcate	accTTGGGC	AGGAACCCG	QTCCAAGGG	TOACACAGC	GGTGATGGC	заватсят	CAGGCCCGG	Tecrocro	<b>GAGGTCAGA</b>	GTGTATT	TaAggACT	GAAGAGAAC	AACACCCG CVT ACCCAGGAA	TACAAAGAA	TACCCAGCC	GTAATCACA	MG [Q/A] GGGCTGCAG	GOOGLOCAGO
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	CONTIG NUM CONTIG POS		3 5	5	Š	258	484	273	324	ā	241	9	5		Ä	2	139	ŝ	ğ	ž	ŝ	8	710	1369	300	273	0Kg	2	240	2	\$	87	462	245	657	12	8	320	9/3	2	227	679	585	121	\$	1010	1072	34	280	878	Ē	83	317	611	319	158	366	286	700	276	Ē	88	8	1	8	à	26	<u>5</u>	88	<u>\$</u>	202	88	271	8	20	8	918	1046	1543
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$\vdash$	HGNC_ID	VONDEDO	VDNOCES	VOLIDEON	V CONDED	XPNPEP2	XPNPEP2 A	XPNPEP2	XPNPEP2	XPNDEPO	YPADEDS	YDNDEDS	VONDEROY.	20000	ATALERA	X-N-E-Z	XPNPEP2	XPNPEPZ	XPNPEP2	XPNPEP2	XPNPEP2	XPNPEP	XPNPEP2	XPNPEP2	BDKRB1		RAKRRI	Вркаві	ı	١	١	1	1		1	l	١	1	ı	1	١					ı	١	1	1		TACRI		1	Ì	П	Н	١	1	١	1	ı	١	1	I	1	١	١	١	1	1	1	١	1	ĺ	ļ	1	1		
in personal principles	- t	Aminopepocase P (memorane-bound)		1	1	,	1	ł	1	1	1	1	1		- 1	- 1	- 1	- 1	- 1	- 1	- 1	- 1			ŀ	1	ŀ	Ł	1	1	- 1	- 1			ı	ŀ	Ł	ì	1	1	1	ı				1	ı	ı	ı		ı				1	1 1	- 1	ŀ	-1	١,	١	ı	-1	- 1	-1	- 1	ı	ı	١	- 1	. 1	١	- 1	-1	-1	1	- 1	1	١.
	3	Aminopepidae	Aminopolitica	Aminonanida	Aminopolidae	Aminopeoplas	Aminopeptidas	Aminopeoples	Aminopenadas	Aminonantidas	Aminopopticles	Aminopolities	Aminoconficial		The second	ATTINOPHORBIT	Aminopepadas	Aminopepiidae	Amnopeptide	Aminopeptidas	Aminopoptida	Aminopepadan	Aminopepidae	Aminopeptidas	Bradykinin Rec	Brackkinin Rec	Brachkinin Par	Brachkinin Rec	Bradykinin Par	and the Day	DIRCONCIDED HE	Bracykinin Rev	Brachkinin Rec	Bradykinin Rek	Brachkinin Rec	Brachkinin Rac	Brach/cinin Rev	Brandelin Re	Grandinin Bo	Brack Minin De	Brackenin He	Bradykinin Re	Brachkinin Re.	Brachykhrin Rex	Bradykinin Rev	Bracykinin Rec	Bradykinin Rek	Techydnin Re	Tachyldnin Ne.	Techyldnin Re	Techyldrin Re	Techyldrin Re.	Tachyldnin Re.	Tachyldnin Re	Ct Estarage In	C1 Esterase fr.	C1 Esterase Ir.	C1 Esternas Ir.	CI Esterase II	C1 Esterase in	Kalikren 1 (re	Kalkron 1 (78	Kalikran 1 (18	PARIETRIN 1 (18	Common Line	Notificial 1 (Fe	Stagnary Hay	Brechkinin Re	Draghkinin Fax	Brachkinin Rev	Brach/drin Re	DOMESTIC HO	Brachenin	Orachite Ha	Drachy Line	Sharking He	Brachkinin Re	Bradykinin Rev	Brachtenin Rev

Table IV (2 of 2)

Bradykinin Receptor B2				CONTINUE	TLAMP OCH INELIALI	TOTAL OF THE PROPERTY OF THE P		, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	87078	A A	A Front	Non-CD8	-			MM 0006231	1877
Jyka Bil Modeliol De	A NKBR	AF104427	Ĺ	1826 AA(	AAGTGGGAA IC/TI GACTGGGCA	285	929	A SOUNCE	07870	7		1	-			NM 000623.1	2117
	Ī	AE40420	[	١	ķ	563	625	AL355102.2	62738	1	I	200				ARE OCCUPATE	2254
Bradykinin Receptor BZ	Ţ	07840120		T	OTOOTO TOOLOGE	KOA	828	AL355102.2	62801	<	G Exon3		-		-	MM COOCES	
Brachkinin Receptor B2	R	AE104829		1	Addison CA II/O Iddologo	100	607	AC003689.1	68127	°	A Intron14	Non-CDS	-				
Anglotensin Converting Enzyme 2		AE109s1 7	_	٦	TRAMAGAN [C/A] CACA I GGCC	0000	900	A COOPERG 4	A0705	c	T Intron12	Non-CDS	-				
Analotensin Converting Enzyme 2		AE10912 1	10		ATCATAGAT (AG) TAAATATAT	286	979		80649		G Introd	L	-				
Analotensin Conventing Enzyme 2	ACE2 IA	AE10983 1	10		ABTTBACAA [C/G] TTTCACACC	597	620	Accosods.	79,00	,	Т		-				
Analotensin Converting Enzyme 2		E109s4			тавтавс (сл.) тасствет	598	069	AC003008.1	50000	•	Christian	L	-				
Annictoral Converting Enzyme 2	ACE2	AE10945	1	440 GA	GAATGCTAA [T/C] ATAAAGATA	665	(53)	ACCOSOS.	2777	ŀ	Т	L	-				
Analohorah Comering Entime 9		L	18		MATANTO ICITI TTGGCACAC	000	8	ACDIGIOS.)	200	•	T	1	-	144	AAC	AF241254.1	2173
Tallian Bankario District	I	Ļ	-		CAGACAC (A/G) TITITAGGT	100	633	ACX003669.1	64245	4	Т	1					
Angiovensin Convering Enzyme z		1		Ī	OCCUPANTAL PROPERTY.	602	<b>9634</b>	L28101.1	6653	٠	G Introd	Ž	•			10000161	8
Protesse inhibitor 4	1	4	1	T		500	ASK	1.28101.1	6734	o	T Exon2		•	Ĕ		NM 0002101	BBB
Protease Inhibitor 4		4	2	T	-ľ	3	8	28101.1	7821	-	C Intron2	Non-CD8	۰				
Protease Inhibitor 4		AE11043	3	- 1	GAGTTAGA [A/G] CATTAG	900	200		100	•	Τ	L	۰				
Destant Inhibitor 4	Pid.	ŀ	3	369	CCCACAAAC [T/A] GCTTCGG	805	/23	11018	300	•		ļ	-	AGT	AGC	NM 0062151	697
Destant Inhibitor A		AF110a5	Ļ		TOAGCTO IA/GI CTGACCAAATC	909	638	1000	/8/6	1		1					
PERSON II MANUAL A		AE11/hab		ł	AGGATGGC IT/A1 ATCCTCAGA	607	639	26101.1	2732	<	Т	1	,				
Promotion of the party of the p				1	CACAGA IAMI TOTATAGA	908	049	1.28101.1	<b>588</b> 2	1	G 5-IND	NON-CUS	1				
sase inhibitor 4	1	AET 108/		1	Carrotte Con Control	900	841	1.28101.1	2544	<	G S'Flank		۰				
Protease Inhibitor 4	P14 1/	AE11098	4	٦	CCAAAGI IG I/C) GGGGAIAG	8	0,0	10000	0726	c	G SFlank	L	•				
Protesse Inhibitor 4	/ Md	AE11089	•		таттгатті (а/с) аттаттат	610	250	, , ,	1	•	Т	L	-				
Aminoconfidese P (membrane.hound)	(DED)	AE100424			gaccagattaglaggtctggt	858	884	ALUZ3053 1	1	,	1	1					
A STATE OF THE PARTY OF THE PAR	Γ		٤	l	CTAGGGGCTACITCGGACCTT	828	885	AL023853 1	70036	2	V.	1	,				
Charles and the second and the secon	CONTRACTOR	ļ		181	CAGGATGITCICCCAACAGG	098	886	AL023653.1	70620	5	Y INDON		1				
Arminopepagese P (membrane-bound)	T	1	1	ı	CARGRACHICIGAGE	198	867	AL023853 1	95621	٥	lutton/	1	1			1 100001	2880
Anticopedate P (membrane-bound)	T	ļ		ı	CATGGTCCCA/GAGGGGGCCC	962	888	AL023853.1	84097	•	A Exon21	1	-			10000	2000
ATHIODEDICARS P. (INSTITUTION PLOCING)	T	1	ļ		TOTTOGGGGGGTAGGGGA	963	688	AL0236531	84129	0	T Exon21		•			1000	
Aminopeptidase P (memorana-pound)	T	1		3 3	COTTO A COLORADO DA A TOTO O	964	088	AL023653 1	61848	_	C Exon6	4	۰	3	3	1000/24	1
Aminopeptidase P (membrane-bound)	Į	1	1	1	200000000000000000000000000000000000000	OFF	891	1,48231.1	1879	g	A Eron3	_		983	25	NIN COO	3
Brachkinin Receptor B1		AE103s10	7	- 1	SANGG I GCAAGGGGGGCCCCA	200	502	1148281 1	2504	<	G Exon3	L	•				
Bradykinin Receptor 81	BOKRB1 /	AE103s11	7	- 1	TGGGCCCT[G/A]IATANICAC	88	760	11400014	SCHE	-	G Exon3	Ļ	٠				
Brachtchin Receptor B1	BDKRB1	AE103#12	7		rcaaggct/glcaagtgATC	18	280	1,10001	1	e	Т	Ļ	۰		L		
American Receptor B1	BDKRB1	AE103s13	_		SAAGTATC(A/G)GGTAATGGC	8	180	040691.		•	Τ	l	-				
Rectytinin Receptor R1		AE103914	-		DTCTCTTATIOTACACTTCC	698	Ç68	O. Control		ľ	Т	1	-			NM 0008231	2051
Drackfield December 82		AF104s30			TTGTGAGGGATTTAAAGGCA	670	968	AL355102.2	1000	1	2	1	-	SAC	Ş	NM 0006231	47
Ometicals December 80	Ī	AF104s31		ı	gcacagaalT/glccTcAcgAA	971	697	AL365 IQ2.2	08030		Т	ļ	-				
Organic Constitution	Ī	4640499		I.	ACTO ACCTIG/AIAGT ACAGTO	872	896	AL365102.2	88330	3	V .	200					
Discovering Consequence	T	AE104022	-	ı	CTGACCTGAIG/ATTACAGTGAA	673	830	AL365102.2	8834	9	Y muon	1	-			NA COORS 1	2183
Dynamic Medical Disc	T	200000		٢	TREFFECATIONARGETATT	874	008	AL355102 2	62672	٥	EXOUS	1	1			1000000	2187
Bracyvorin Haceptor 62	Ī	ACCOUNT		Τ	TTTCTAGAIC/AICTCAGTGTC	875	106	AL365102.2	62685	٥	A Exon3	4				100000	4012
Bradyonin Heceptor BZ	1	2	,	Τ	O SOUTH CONTROL OF THE OWNER OF THE OWNER	878	208	IAL365102.2	62943	0	A Exon3	3 Non-CD8	-			100000	
Brachkinin Receptor B2.	286	AE104838	0	Т	ACCRICATION OF THE PROPERTY OF	243	808	1.28101.1	9169	o	G Exon4	4 Sient	۰	YGG	VQQ	NM 006215 1	2
Protease Inhibitor 4.	Pk	AE110e10		1	Macilardana	100	28	1 20101	3812	0	T Exon	4 Missense	•	CGC	gg	NM 0062151	412
Protesse Inhibitor 4	P.4	AE110811	•	-1	CACGCAVGIIGITICS	0/0	300	1 28101 1	2624	٥	T 5 Flank	Non-CDS	•				
Protesse Inhibitor 4	P.4	AE110812	+	1	GTACCGG/AITTCATAA	8/0	200	400074003	141072	e	A	Non-CDS	-				
Tachyldin Receptor 1	TACR1	AE106s8	5	85 85	ATGTAGATIAAGGTCTTGTGG	200	806	4 0007400 9	14996	,	A Inhons	L	-				
Fachvidrin Recentor 1	TACR1	AE108s9			CCAGA[T/G]GCAGCTAG	88	901	C.004 (000)	20,04		T	L	-				
Andolensin Contacting Forting 9	ACE2	AE109a8	12		TTGTGACAACA	882	906	ACMISSION	0/400	,	T	SOC SON	-				
Analohous Compating Engine 2	200	-	1	l	AGTACATTCGAAGAATT	883	808	AC003669.1	9000	•		4					

	5 65	Г	and others are and	AN CORRECT IN ANY CORRECT	RESSED ELANX	REFSEQ FLANK REF (SEQ ID NO.) REF	REFSEQ ALT (SEQ 10 NO.)	DEF SEO ID	REF SEO POS	REF. NT ALT NT	EXON MUTATION	MUTATION TYPE REVCOMP	圛		9	CONA SEQ POS
Aminosophese Ofmenters by the Man	TONOCOS ACTORES		1 127	1_	aATGTCAGCCTGCTGTCTCCCCGAGAGCATGTGAGTGCCCCTCA		88	AL023853.1		0	Enorgo Saler	٩	8	900	U00724.1	\$365
		_	8	ž	атстосттвовамсявтостратеттясястваятссявт	181	727	AL023653 1	80150	-	Intron3 Non-CDS	o S	1			
Γ	П		224	ž	COAGATTTCCCCTCACCACGTICTCCCCCAAGGGGGCCCAA	591	822	AL0238531	74483	+		90				
	Τ-		36	-	вессиставсиси в в в в в в в в в в в в в в в в в	168	622	AL0238531	74651	9		98	_		1	
	П		22	-	маммаааттааматамааатиствавасссаматстстттт	167	82	AL023653 1	54549	٥ ۲	Intron 1 Non-CD8	98		1	1	T
	П		200	-	ARCACTOCCAGGCCACCCIC/TCTT/ATTATACCCTCTATG	168	122	AL023653.1	76521	0	Intron7 Non-CDS	8				
	XPNPEP2 AE10087	,	194	××	ттаттамадаммадаттісластастттимамадатас	169	222	AL023653 1	65566	0		80				
	XPNPEP2 AE10018		13	-	CCTGCCAGTCCTCTGAAAAGAGICCCCTGTGCCATGGAGACCT	170	233	AL023653 1	98289	4		80 98				-
Aminopepidase P (membrane-bound) XPN	KPNPEP2 AE10049		13 324	-	тавлаласьттаросьствальный при	171	22	AL023653 1	98238	- 6	neporto Non-Colo					
		9	+	٠	TTGCAAACCTTAGCATGCACCGTGAGTCACCTGGGATGCTTG	225	8	AL023653 1	2,008	┾	1	3 2				
	- 1	=	+	¥¥.	GAAGCCCAGGCCCCAGAGGTTCTTCCCCACCAAGGCCTCCCAC	173	<b>8</b>	ALUCCORDS I	Den't	-   •	L	2 2				
T	Т	2	+	8	ABBCCCCABABBTCCTCCCAICTICAABBCCTCCCACGTGACCC	174	/62	ALUCADAS.	71057		Month	80	_			
T	- 1	<u>_</u>	28	0	GGCCTCCCACGTGACCCAGTGACAGGGTTAGGCTGCCTTCT	1/3	88	A1 0020000.1	64058		Fanot Mon-CD8	0				
T	Т	<u> </u>	22	¥¥.	gawagacctawagawagacjccagagawagagcctcct	9/1	ACC.	AL OTOMES 4	7	╁	L	8				
T	Т	2	+	-	Accetetateracica accepting a Angle and a A	,,,		41000000	70000	╀	L					
		9	+	-	CTTGCCTCAGGCAGATCAGCAGGTTAAATATTCCTTGTCAATT	178	183	ALUCADA.	*****	,	Ļ	-				
1	- 1	17	+	-	ACTGATACCATGTTTATGTCTTGTTCTTTCTAGGGCCAGTGGG	677	382	A GC 2003	1000		J.	3 8				
Aminopepidase P (membrane-bound) XPN	XPNPEPZ AE100s18	92	22	1	AATAAATAATAAAAGCCAGIACGCCAATCTGGTGTGTGCCAG	190	243	AL023653.1	77052	+	Introni / Non-CLO	+	-			
Aminopeoplease P (membrane-bound) XPN	XPNPEP2 AE100s19	18	38	1	GTCCTGTGGGTCCTCCCGGAITCCTCCATATCACCTCTTCC	181	75	AL023653.1	75689	y (	Infront b Non-CLUS	+				
Aminopeolidase P (membrane-bound) XPN	XPNPEP2 AE100420	8	27 308	0	АССТСТТВВСАВСТТВВСТПАЛВІВАВВВСТВТСАССССТТСТ	291	545	ALC23653.1	83468	╀		5 1	-			
Animosepidase P (membrane-bound) XPN	XPNPEP2 AE100421	2	27	¥	сстатавадандартссоловислаксславалисленда сттст	163	246	A.0238531	63828	0	Exercit Non-City	+				
Antinopeoticiase P (membrane-bound) XPN	XPNPEP2 AE100422	8	238 710	0	CCGGGGTTGTATACCACACCCCGTTGGGGCCCTAATCCCAGGCC	184	247	AL023853.1	83858		1	+				
Aminosepidase P (membrane-bound) XPN	XPNPEP2 AE100423	8	38 (300	0	смаяталассласиттсслаютпеттслессттеласимся	186	846	W 023653 1	84585	0	_	$\frac{1}{1}$		1		
Bradykinin Receptor B1 BCK	7		907	0	ANTITATOTTTO TO BOOK OF THE TOWN OF THE TANK OF THE TA	186	546	U48231.1	2307	+	Exorg Miseriae	1	200	3	NM 000710 1	8
Bradykinin Receptor B1 BDK	BDKRB1 AE10362	9	4 273	-	CTBCTBCACABABTBCTBCQQAAACATTTATCATGTGCATGTB	187	350	U48231 1	1380	+	1	+	8	Т	101/000 MW	2
Bradykinin Receptor B1 BDK	$\neg$		7 958	1	<b>АЗАМВСТТВВСТТТСТАТСРАВДТТСТТВТВАСАТААТАА</b>	188	152	U48231 1	9582	θ	1	8				
Brachkinin Receptor B1 BDK	BDKRB1 AE10344	4	- 18	1	таттатталамсмавалстисматссатсваессмамот	199	282	U48231.1	88	5	Exert Non-CDS	80				
Bradykinin Receptor B1 BDK	BOKRB1 AE10315	•	7 240	-	ATABTECTAGGATTATAGGCGVATGGCCACTGCCCCTGGCCCC	280	283	U48231 1	3072	9	Exercit Non-CD8	88				ľ
Bradyfurm Receptor B2 BDK	BDKRB2 AE10441	_	88	NA.	CANATOTECAGGGTCCCCCCCGNGNCCGCCCCAGGTGGGCCCC	161	584	At 356102.2	98426	9	Intron Non-CD8	- 88	1			
Bradyform Receptor B2 BDK	BOKRB2 AE10442	2	10 87	0	<u> матетасададетсесссима</u> нсеведессаватадаесесет	22	2922	AL 365102.2	98427	4	1	80	-			
Brachtbrin Receptor B2	BOKING AE10443	<u>_</u>	10	0	ANGGGTGGGTGAGGTCATGT/AITCCCCTCTGAGACTCAGTT	8	286	AL365102.2	208803	<b>₹</b>	Intraut Non-CD8	1				
Brachtinin Receptor B2	BDKRB2 AE10444	4	10	0	слеваленаествеалталениестиствеван	194	257	AL365102.2	28883			20	1			
Brachdonin Receptor B2 BDK	Т		10	0	Толевестваватастаесполятваваласасасатаетт	198	258	AL355102.2	26897	9	introni Non-COS	- ·				
	Т		712	ž	TGCTGCCAGGGCCCAMGAGGAKAGCACAGTTTTTCTCCAG	198	8	4300106.2	9000	9 0	Month Month	3 8	-			
	Т		2		(accetegaagaagaagaagacittatagaacacaagacttaga	701	8	AL 200106.2	63000	3 4	County Monchy	3 6			NM 000623 1	2002
	BUNNESZ AETONE		e :		TOOLS TO THE OUT OF THE OUT OUT OF THE OUT OUT OF THE OUT	8	96	A1 265102 2	80238	-	Exerd Non-COS	- 88			NM_000623.1	2117
DANSON THE STATE OF THE STATE O	BUNNES AFIGHE				TOTAL DESCRIPTION OF THE PROPERTY OF THE PROPE	82	2	AL 345102 2	10909	9	L	- 88			NM 000623.1	75.2
	T				ATARCAGETCATTOACTETTTOCACAGACAGATGTTCTTA	8	ž	At 365102 2	25113	-	Expris Non-CDS	1			NM 000623.1	3804
and the second s	Т		ŀ		COTTATOA DE TITOA CA DE CANADA DA CANADA DE CONTRATOR DE	8	*	At 355102.2	61138	9	Expris Non-CD8	1 90			NM 000623.1	3508
	Т		2	2 2	AAGAGAGTCTCAGCATCACCTCTGCTCTGGTGCTGAATGAC	88	566	AL365102.2	61280	0	Exert Non-CDS	1 10			NAM 0006231	3466
	Т	<u> </u>		***	account of the second s	28	292	AL355102.2	08229	0	L	1 50			NM 0006231	2565
	1	ļ	0 1		TOTOLOGICA		5%	A 255100.0	60403	6	L	50				
	Т		ł		TO A CONTROL OF THE PROPERTY O	800	200	Ai 365102.2	1409	0	L	- 80				
Transferin Description	TACO.	<u> </u>	200		OCCARDACANCHOCOSTOCATOGRAPHICA CONTROLA	202	230	AC007681.3	103665	4		-	ш	ΣĽ	NM 0010582	88
			8	420	ASCARGAGAGAGAGAGAGAGATATAGACAGAATAACACATTT	88	12	AC0078813	25759	6	L	-	ATC	ATA	NM 0010682	672
			$\vdash$	٥	аватаваттивтогостативсостасисистивсаетт	â	212	AC007400.3	143458	٦ 1	Intend Non-CDS	- 80				
	CR1 AE10844	2	\$ \$	0	CAGAATGGAATGAATGGGCTTIYCITTGGGAAAAGCTGGTCCCGAC	210	273	AC007400.3	139028	°	Exons Non-CDS	1				
	TACR1 AE10845	, g	6 220	0	CARTOATTTOOTTTOAGTCACCAACACCATGAGGGTGGCAAAG	211	274	AC007400.3	139096	3	Exon\$ Non-CDS	108	4		NW 0010582	929
			5 317	¥	CTGACCCTTTTTGCAAGTCCCTAGTGTGAGGGTGTTCTGAT	212	275	AC007400.3	139193	9	Exert Non-CDS	500	$\downarrow$		NA 0010582	888
Tachyldrin Receptor 1	TACR1 AE10867	-	6 511	•	ттвамавтсмавтесмавамстрмавататавсеттававсе	213	278	AC007400.3	130387	0	Exon5	E	ğ	ğ	NW 0010882	100
C1 Esterare Inhibitor	NH AE105s1	-	3 319	٥	састававаллавалсивиливалитаттавластасла	214	112	X34486 1	5756	9	1	+	1	1		
C) Esterage Inhibitor	NH AE10542	2	5	0	GCGGTAGGAAGTGTTAAGAGTGCATCTCTATTTTCTAGG	215	273	X54486 1	15183	V	1	$\frac{1}{1}$		!		8000
	T		+	٥	CGCATCAAAGTGACGACCAGICTICAGGATATGGTCTCAATCAT	216	22.0	X84498.1	1540	4	Examy Swear	E .	1	1	MAL COOCUES 4	202
	T	1	+	8	TATCTCCAAGATGCTATTCGTTGAACCCATCCTGGGAGGTTT	702	200	Verient.	2000	, ,	Emes		ş	₹8	N#4 000062.1	983
CI Estação Inhibator	MH AETOSAS	9 1	i i	0 14	TAPAGE ACCOUNT OF THE PROPERTY	816	28	X54456 1	18012	0	Exord May		ата	ATG	NM 000062 1	1498
1		,	ł	-	TOCTOCCTAATOATOATOCACACACACACACACACACACA	8	282	AP277050 1	£	٥	Exp./	0	VVV	g/A	NM 002257 1	285
		,	8	-	CARACTOTOTAGCCAAAACAAAAAATAAAATAAAACTCCTGCGTC	ā	762	AF277060 1	4627	θ		0 800				
Γ			)		AGGTCGTGGAGTTGCCCACCTGCMGGAACCCCAAGTGGGGAGC	222	285	AF277050 1	4532	9	Exons Muserse	0	GAG	8	NM 002257.1	69
		3	H	0	адсададатадададстоторутосья в дамини в доста	200	286	AF277050 1	4	0	Intend Non-CDS	902	-	1		
		92	4 625	-	<u>вевесиссеветататемиятетемиваматетам</u>	224	282	AF277050 1	88	4	3 Flenk Non-CD9	8	-	1		
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	T	-	-	¥¥.	стестетассатателементраваятелемавасемятт	643	878	U482311	35	0 0	Expr.3 Silveri	e .	¥ 5	\$ 5	NA 0007101	£ 5
	1	9	-	0	даммаасмасмасаасаама[ам]смаасссааатсмостарат	844	E 1	1 2 2	E .	5 (	Ļ	+	2 5	a a	NA 000710.1	22.5
Bradytonn Receptor 81	BOKRB1 AE10348	9	-	٥	Tambatcacogoriocatologilociocitoxocoatiavagaco		2/6	(Mages 11)	loso	┨	Elero I	-				

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Bradylánin Receptor B1	Y IBLYOS	AE103e0	7	961	0	асстсоствовалсвовваналуваветслеслевалслалет	958	678			0	E BOO	200	0	GAG	NO.	GAA NAM GOOTIO.1	705
CRIPTION		J	CONTING HUM CONTING POS	SON TIG POS	REFSEQ FLANK ORIENT	RETSEO FLANK	REFSEO PLANKREF (SEQ ID NO. )	REFSEC ALT (SEC) ID NO: 1	BEF SEO ID	REF 8EQ POS		T fotment of	MONTH IN	WEAVOUR.		1	THE SECTION	20 1 NOW WORK
	T	AE104s18	+	2		CTGGGGATTGCAAAATACAGGTTCATCTCCAGCAGGGAGGAA	8	4/6	AI DEELING O	49077		Fmo	Manna	-	CGT	Ē	NM 000623.1	9
	Т	AE104s19	†	88	-	GGTGGGGCCGGGAGTCCTCACGCAAACAGAACATTGATA		100	AI DERING O	101078	H	S. Flank	Non-CO8	-		Γ		
	Ť	AE104620	+	ī.	WA.	ABCCTTAMACCCTTCCTTC/AC/CAA/GACAGATAAAABIB	ŝ	8	A1 000 100 0	ozero,	•	Т	Non-CO8	-				
	Т	AE104621		8		Address of the content of the conten	96	5	A1 945100 2	10000	-	✝¯	Non-CD8	-	-			
	Т	AE104622	ļ.	2 :		Adjuctional programme and added to come and a contract of the	69	789	AI 345102 2	100381	9	A 5Flank	Non-CD9	-				
Dracyteran Heospool 62	SIX HES	ACTOMICS		8 8		GARGERATETRATATATATATATATATATATATATATATATATA	28	685	AL355102.2	63922	~	G Exond	Silent		PAT	T	NM 000623 1	83
		AC10100	-	970	-	Tagatteraceracidencescentificageacacactecerag	3	989	AL365102.2	63794	0	T Exond	Mesonse	-	990	GAG	NM 0006231	1061
	Т	AFIDACM		3	-	тасассамаставатавсімаюттетествалаттеталат	625	687	AL365102.2	63297	<	G Evens	Non-CD8	-			NM 000823 1	1568
	П	45104-07	-	1828	-	автратавскатасссивтовинтессисттамететтама	929	688	AL365102.2	62978		A Exond	Non-CD8	-		1	NM 0006231	1677
	Г	AE104628		88		TCCCAGTTACGTCTGCGTANTIANATGCCTCACATGTACGTAG	299	686	AL365102.2	862238	٢	A Front	Non-CD9	-		1	NM 000623 1	2117
	Г	AE104/29		982	-	талславтваливаниссилителениестепривоси	959	088	AL365102.2	62601	1	6 Faord	Non-CDS	-		7	NM 000823.1	752
Enzyme 2		AE109e1	_	2	0	ACTIATABITITIQAAAAAAACAICACATGGCCTCTCTTC	659	168	AC005869.1	72189	ü	A Introduct 4	Non-CD8	-				
		AE10942	9	22	,	TCCABATGTACATATATTACCTATGATCTATGATCTATGGTTTCT	98	2893	AC003669 1	98,000	ő	T Intronti2	Non-CDS					
_		AE10943	٥	88	-	алсливалитавататаллистоттатслиствавтетистся	\$8	289	AC003689 1	88842	+	G Intron13	Non-CDS	-				
		AE1094	=	26	0	CACTACTAAAAATTABTABGGCTTTAGCTBBTTCAAGTAATAAB	36	169	AC003669 1	190184	٥	T	Non-CD8	-				
		AE10945	Ξ	\$	0	TTTGCTGAAGAAATGCTAATICATAAAAATATGCTTTTGACC	883	969	AC000969,1	22008	+	C Introd	Non-c08	-				
		AE109e8	5	80	0	OTAMATGACTCAGAATAATG C/TITTGGCACACAGGAAAAAACAC	984	989	AC0000689 1	64113	9	T Intront6	Non-CD8	-		T		
	ACE2 A	AE109s7	5	343	•	CTABBANTBANTACABACACIA/BITTTTABBTBCABTBACAAA	999	200	AC003669 1	84245	+	7	Silent	-	TM.	S N	AF241254 1	2173
		AE110s1	2	74		CTABOTOTATAGCOTBCAGAT/A019TOCTBTACCTTCTTTCAT	989	86	1.28101.1	8993	+	G Intron1	Non-CD8	۰		Т		
		AE110e2	2	929	0	ASSACCACTCCCAAASACTTICTTTATGTTGATGAGAACACAAC	.88	889	1281011	6734	+	T Emorg	Silent		Ë	F	NM 0062151	8
		A£110#3		168	•	actretroattateraterremenaceaatecocottic	88	82	1.20105.1	1881	-	C Ambord	Non-CDS	•				
		AE110M	•	592	-	GAGGTGTGTGAGCCGAAGCT/AKITTGTGGGGGACAGAACTCA	698	701	128101.1	77.20	+	┪	Non-CDS	•		7		
		AE11045	,	583		ANGATTGTGGATTTGGTCAGTTCAAGAAGGACGTCTT	670	702	128101.1	3797	-	CExon	Silent		AGT	AGC	NM 006215.1	260
		AE11046	,	6291		CTANATAAACTCTGAGGATJATJGCCATGCTCCATGCAAAATC	1,10	202	138101 3	2772	<	T SFlank	Non-CD8	•				
		AE110a7	,	1965	ĵ	сататааласастссасаадпарттатавалсаалсостал	872	ğ	1381011	\$6 \$6	-	6 S'Plank	Non-COS					
		A£110eB	,	1816		COORDINGCAATTCTATCCCCIANOICAACTTTBGGCAGGTCACTT	613	æ	1381011	284	<	G S'Flank	Non-CD8	•				-
		AE11040	,	3050	1	CAMCAAACAAACAACCAAAAAAAAAAAAAAAAAAAAAAA	7/0	ž	138101.1	953	٥	G 5'Berk	Non-CD9	•				
membrane-bound)	2434	AE100424	•	363	,	CTGTGGCTGCAACCAGACCTIC/TACCCGGGCTCCTCTGTTTCCC	910	908	AL023853.1	1788	3	T Infronti	Non-CD8	-				
	XPNPEP2	AE100425	13	83	-	<u> матесисаттам в втесвија и и у и и и и и и и и и и и и и и и и </u>	911	703	AL023653.1	70896	0	A kntron13	Non-CD8	•				
	·	AE100#26	13	101	-	тттстававсстаттавајскасктостаттатататама	612	908	AL023653 1	70820	•	A Intronf3	Non-CDB	•				
	ļ	AE100427	18	112	0	<b>АМВВСТВОСАТЕ В В В В В В В В В В В В В В В В В В В</b>	913	882	AL023653 1	65621	٥	Tutton/	Non-CDS	•				
Aminopeopidase P (membrane-bound)	XPNPEP2	AE100s28	24	381	0	CCCAAGGGTGCCATGGTCCCGGAAGGAGGCCCAAACCTATCAC	\$10	OF6	AL023653.1	84097	8	A Eworg1	Non-CD8	•			U80724 1	3880
		AE100429	53	883	0	<u> дестателеслеттавателитивесламаетаттеселе</u>	916	1140	AL023853.1	64129	٥	T Exorg1	Non-CDS	4			U80724 1	2801
		AE100430	22	2	-	TGBCTCCTCACCGAGATTCCT//CRGTGAAGGGCGTGTGGGTTT	916	942	AL023653 1	81848	-	C Exore	Silent	٥	55	Τ	U80724.1	71
Bradyldrain Receptor B1	BDKR81	AE103s10	,	788	0	аатслаславления таста сполива в в сели в в в в в в в в в в в в в в в в в в в	917	88	1482311	atot	•	7	Missense	•	993	8	NA 0007101	128
Bradykinin Receptor B1	Ť	AE103s11	-	282	0	алаттатсславтвавссоцивітаталслоливавтостта	948	£	U48231.1	5604	1	Т	Non-CDS	•				
Bradykinin Receptor B1	BOKRBI	AE103412	7	1808	0	стватстсимстсимавасциарсиматалтестосисттва	916	88	U482311	9000	-	6 Exercis	Non-CDS	•		Ī		
	T	AE103e13	_	1946	6	GGAAACAAATAACAAGTATCGAAGGTAATGGCCTCTCTTATTA	88	848	1821			┰	NON-CUS					
	Т	AE103e14	,	1961	0	TCGGGTAATGGCCTCTCTTATICITACACTTCCATTGTCTATT	126	ž	1823	I I	ļ.	SUCCE S	Non-cus				ATT COOK	506
	Т	AE104630	~	28	1	АТАССТВТІАСТВООТТІЛАІСТІОСТСАСАЛОВАСТІСАТВТТ	258	948	AL 365 102 2	10828	0	Т	Non-cus	-	350	٤	NE COOCS	20
	Т	AE104e31		8	0	давосетветевесисавдетивостсиовисивиче девосетветевесисавдетивостсиовисивиче	226	93	AL365102.2	06089	‡	G Exord	Mesense Man one	1.	3	3	W COOPERS I	F
	Т	AE104e32	-	402	0	TAATAACTGCAAACTGACCTGAAAAATACAGTGAAAAATCAAGC	728	98	AL309102.2	96539	,	A STATE	North Office and a second	1				
	Т	AE104#33	•	ş	0	ATAACTECAAACTEACCTEA(BATTACAETEAAAAATCAAECAA	226	ŝ	A.50106.4	9604	,	The state of	Star Cho				NM 000623 1	2183
	Т	AE104634		<b>8</b>	0	CCANACTGATTCTGCTCCAICTTGGAGCTALTCTAGACCTCA	25	2 2	At SER (PO O	9000	, ,	7	Non-CD8	ļ. Ļ			NM 000823.1	2167
	Т	AE104835		ž :	0	Secondary Control of C	2 5	3	AI SKAIND 2	UNO.		A Exord	Non-CD8	-			NM_0008231	1912
88	BILKINGS	AETUMESO		200		CONTROL OF THE PROPERTY OF THE	8	ž	28101.1	0160		G Front	Sien	۰	YCC	ACG	NM_0082151	1143
Process by the A	T	ACTIONS		ě		CONSIDERATION OF THE PROPERTY	8	956	1281011	3812	0	T Emont	Missense	٥	Sgo	TGC	NM 0082151	412
		ACTIONS		600	-	GACAGATGTTCATTATGAAAIC/TRIGGTACCAATTCTATCCCCA	ē	298	1,28101,1	5824	0	T 5' Flank	Non-COS	۰				
	į	ACTORES		8		тавсовствутататаванска подпосости	288	88	AC007400.3	141073	6	A Intron4	Non-CDS	-				
		AFINES	١.	*	-	GAATATTTETECTAGCTGCCATTCTGGGGCTCACAGTGTGC	808	356	AC007400.3	143386	υ	A Intrort3	Non-CDS					
Forms 2	Γ	AF10948	2	9,		AAAAAAACATTCTCAGCTGTTGATTCACAAGTCCTCATGAGACT	28	086	AC003689 1	69475	9	T Intront3	Non-CDS	-				
	П	AE10949	8	23	0	АТАКСАМВАВССАМВТАСА[СТ]ВАМВААТТСАТВВВВЕСТТСТ	505	ě	AC003689 1	82668	0	T Introne	Non-cos					
5		AE10742	-	88	0	аясославая тоссоятос (сл. сосоттовает яследа	1574	1576	AF277050 1	4627	0	A introns	Non-CD8	¥				

MOLEGICOSCO SECONO	CNON	C CNO	or one of one	Š	REE AA	AT T AA	NOX	MUTATION TYPE REVCOMP REF CODON ALT CODON	EVCOMP	EF CODON AL	T CODON P	PROTEIN ID	PROTEIN_POS	NO: )	(SEQ ID NO:)	(SEQ ID NO: )	(SEQ ID NO: )
Aminomentidase D'inamhrana-houndi YPNPEP2 &E100s1	YPNDEP	AF100e1	-		٩	-		Eass		200		AAB96394,1	607	4	37	100	163
Brachkinin Becantor B1	BDKRB1 AF103s1	AF10381		307	æ		Exon2	Missense	0	000	CAG	NP_000701.1	317	8	98	123	186
Bradykinin Receptor B1	BDKBB1	AE10382	4	273	۵.		Exon2	Silent	0	cca	CCA	NP_000701.1	41	10	5	124	187
Tachvidnin Becentor 1	TACR1		-	614	<u> </u>	u.	Exont	Silent	-	ш	TTC	NP_001049.1	111	91	8	144	207
	TACRI	AE106s2	2	789	-	_	Exon2	Silent	-	ATC	ATA	NP_001049.1	164	82	85	145	208
	TACRI	AE106s7	ø	511	6	ø	Exons	Silent	-	TCG	TCA	NP 001049.1	378	8	87	150	213
C1 Esterase Inhibitor	H. I	AE10583	G	366	v	s	Exon7	Silent	0	AGC	AGT	NP_000053.1	406	58	8	153	216
C1 Esterase Inhibitor	CINH	AE10584	7	588	>		Exon3	Missense	٥	атт	GCT	NP_000053.1	28	82	8	154	217
C1 Esterase Inhibitor	E S	AE10585	7	268	⋖	9	Exon3	Missense	0	GCA	GGA N	NP_0000531	159	28	28	155	218
C. Esterase inhibitor	TX.	AE10586	•	276	>	2	Exon8	Missense	0	ата	ATG	NP_000053.1	480	90	83	156	219
Kallikrain 1 (ranal/hancraas/kalivary)	K	AF107a1	-	153	×		Exon4	Missense	۰	VV	GAA	NP_002248 1	186	æ	94	157	220
1	<u> </u>	AF10783		902	ш	$\Box$	Exon3	Missense	0	GAG	CAG	NP_002248.1	145	88	98	159	222
1	8DKR81	_	-	87	2	Ι"	Exon3	Silent	٥	AAC	AAT	NP_000701.1	114	556	629	611	643
Brachkinin Receptor B1	BOKRBI		-	19	Œ		Exon3	Slent	0	AGG	AGA	NP_000701.1	152	558	280	612	644
Bradvkirtin Receptor Bt	BOKRB1	BDKRB1 AE10398	-	596	ر	>	Exon3	Missense	0	ств	GTG	NP_000701.1	191	999	581	613	645
Brachkinin Receptor B1	BOKRB1	BDKRB1 AE10389	a	8	ш	ш	Exon3	Silent	0	GAG	GAA	NP_000701.1	233	562	285	614	648
Brachkinin Recentor 82	BOKBB	BDKRR2 AE104819		88	œ	٥	Exon2	Missense	-	СВТ	TOT	NP_000614.1	14	299	584	616	648
Brackfelin Recentor R2	BOKBR	RDKRR9 AF104604	4	918	٦		Exon3	S S S S S S S S S S S S S S S S S S S	-	GAT.	GAC	NP_000614.1	311	999	689	621	663
Bradykinin Receptor B2	BOKRB2	BDKRB2 AE104625	4	1046	ø	l	Exon3	Missense	-	999	GAG	NP_000614.1	354	568	280	229	654
Analotensin Converting Enzyme 2	ACE2	AE10987	15	241	z		Exon16	Silent	-	AAT	AAC /	AAF78220.1	069	843	109	623	999
Protease inhibitor 4	7	AE11082	2	528	u	u.	Exon2	Silent	0	TTC	E	NP_006208.1	233	574	603	989	667
						Γ										_	

	<211> <212>	1576 34 DNA Homo sapiens	
	<400> gcagcag	1576 gegg cegeetgeac agagtgetge egae	34
	<211> <212>	1577 34 DNA Homo sapiens	
	<400> gcagca	1577 gtcg acattccgcc agaaaagttg gaag	34
The state of the s	<210> <211> <212> <213>	1578 39 DNA Homo sapiens	
The state	<400> gcagca	1578 agcgg ccgcatggca tcatcctggc cccctctag	39
	<211> <212>		
1000, 1000 1000, 1000 1000, 1000 1000, 1000 1000, 1000 1000, 1000 1000, 1000 1000, 1000 1000, 1000 1000	<400> gcago	· 1579 cagtog acaaagaagt tggccaattg caggccc	37

Table VIIA

DNA panel	Coriell Catalog #	Sample Description XPNF	XPNPEP2 BDKRB1 BDKRB2	32 TACR1	C1NH	KLK1	P14	ACE2
Coriel 24 panel	NA14905	African American 🗴	×	×	×	0.47******		
Coriell 24 panel	NA14922	African American X	*	*	×	20008-4		
Coriell 24 panel	NA14923	African American 🗴	× ×	×	*	WALCO E		
	NA14924	African American x	× ×	×	×	1. 200000		
panel	NA14925	African American X	×	×	*	NR:000 X		
24 panel	NA14932	African American 🗴 💮	×	×	×	200.000.000		
24 panel	NA14933	African American	<b>x</b>	×	×	someon"		
	NA14934	African American	*	×	×	50000		
24 panel	NA 17201	Caucasian	* *	×	×			
	NA17202	Caucasian	×	×	×	200.751		
	NA17203	Caucasian	×	×	×	K>640		
24 panel	NA17204	Caucasian	× ×	×	*	087153		
24 panel	NA17205	Caucasian	×	*	×	(5-280)		
24 panel	NA17206	Caucasian	×	×	*	\$58.9°		
24 panel	NA17207	Caucasian *	×	×	×			
24 panel	NA17208	Caucasian X	×	×	×			
24 panel	NA00576	Chinese	. ×	×	*			
	NA03433	Chinese	× ×	×	*			
panel	NA06090	Chinese	*	×	×	****		
24 panel	NA07426	Chinese	×	*	*			
24 panel	NA02345b	Japanese	*	×	*			
24 panel	NA11589	Japanese 🗴	× ×	*	×			
	NA14819	Japanese	×	×	×	625		
24 panel	NA04535	Japanese	×	×	×			
STATE OF THE PARTY	NA14672	African American						
Shellel A	NA14682	African American					,	
S panelate to the	NA14683	African American					1	
	NA14696	African American						
More line Supplied in the control of	NA14698	African American						
legines (sulferior)	NA14700	African American						
A POST OF STATE OF ST	NA14704	African American						
MD 50 AA panel 25 Mills	NA1850	African American						
HD/ S0/AAC parelet - Free	3382	African American						
ED do AA panel and as as	3725	African American						
	6865	African American						
	7754	African American						
FID 50 AA BRIDE SE	10251	African American						
	10378	African American						
MD 50 AA panela See Co	12931	African American						
HD 50 4A panel a service	13294	African American						
HID on An panel of the	14439	African American	1					
HD SO AS BATELL STATES	14441	African American						
MD 40 A A panelos 1455	14454	African American 🔏						
HID SIC AND JUNE 19 TO THE	14464	African American						

Table VIIB

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2 BDKRB1	BDKRB2	TACRI	CINH	KLK1	P14	ACE2
	14537	African American	×						
HD 50 AA nanal	14583	African American							
	14681	African American							
	14001	African American							
Jane I	1400/	Africal American							
sanei	1469/	Amcan American							
Danel	14699	African American							
anel	14720	African American							
	14746	African American							
50 AA nanel	14754	African American							
	14755	African American							
HO FO A panel A CH	14771	African American							
	14772	African American							
	44700	African American							
Halled www.ca.du	14703	African American							
halle!	14050	Allican Allicano							
panel	14837	African American							
	14862	African American							
	14863	African American							
HD 50 AA panel	14864	African American							
	14892	African American							
	14893	African American							
lone	14894	African American							
	14895	African American							
D.	14007	African American							
ou AA panel	1489/	Assican American							
AA, panel	14900	African American							
i0 AA panel	14901	African American							
MD 50.44 panel	14903	African American							
HD 50 AA panel han his	14904	African American							
	14905	African American							
60 A	14922	African American							
HD 50 AA panel	14923	African American							
HD 50.4A panel 37 see at	14924	African American							
HD BOAA DARM	14925	African American							
MD 50 AA caneli a	14932	African American							
FID 50 AA sanel	14933	African American							
HD CONCALL Banel & St. 12	NA 17201	Caucasian							
An Tombour name	_	Caucasian							
FID: FOLD GALL management was	17203	Caucasian							
an Strate Co. Her grad	17204	Caucasian							
Him to the All mande	17205	Caucasian							
HP TOTAL STREET	17206	Caucasian							
With the property of the prope	17207	Caucasian							
The state of the s	17208	Caucasian							
All the second of the second o	17209	Caucasian							
	17210	Caucasian		358					

## rable VIIC

DNA panel	Coriell Catalog #	Sample Description X	XPNPEP2 BDKRB1 BDKRB2 TACR1	R1 CINH	KLK1	P14	ACE2
PD 100 GAU panel	17211	Caucasian	***				
MD 100 CALIDADA	17212	Caucasian					
HD 100 CALibanel Inch	17213	Caucasian					
HD 100 CAU panel To the	17214	Caucasian					
	17215	Caucasian					
seya.	17216	Caucasian					
HD, 100 CAU panel	17217	Caucasian					
	17218	Caucasian					
ಜಿಎಡ್	17219	Caucasian					
<b>X</b> & 3	17220	Caucasian					
(X) 2000	17221	Caucasian					
	17222	Caucasian	a l				
Sistem S	17223	Caucasian	*				
HID 100 CAU panel - 2	17224	Caucasian	e e e				
53V-233	17225	Caucasian					
	17226	Caucasian	- III				
HD 100 CAU panel.	17227	Caucasian					
	17228	Caucasian					
HD 100 CAU panel	17229	Caucasian					
	17230	Caucasian					
888 W.	17231	Caucasian					
100 CAU	17232	Caucasian					
	17233	Caucasian					
FID:100 CAUpane)	17234	Caucasian	*				
MD 100 CAU panel 35 7	17235	Caucasian					
HD 100 CAU panel	17236	Caucasian					
HD 100 GAU panell et 🤝	17237	Caucasian					
MD 100 CAU panel 🥦 💀	17238	Caucasian					
MD 100 CAU panel	17239	Caucasian					
HD 100 GAU panel	17240	Caucasian					
MD 100 GAU panels 🖘	17241	Caucasian					
HD 100 CAU panel 188	17242	Caucasian					
ellos eves barres	17243	Caucasian					
	1/244	Caucasian					
HIM OF SAUDING	1/245	Caucasian					
Elegion Consisted	17246	Caucasian					
MO-100.CAU panel 2.3%	17247	Caucasian	•				
ISID TOTICALL participation	17248	Caucasian					
Market CAR plane	17249	Caucasian					
Hills for GAU puneling	17250	Caucasian					
	17251	Caucasian					
The Participant of the Participa	17252	Caucasian					
	17253	Caucasian					
MID: TOR GATE BENGING A	17254	Caucasian					

	# 20]e+a0   c =a0	Semple Description XPNPFP2	Table VIID XPNPFP2 BDKRB1 BDKRB2 TACR1	C1NH KLK1 PI4 ACE2
DNA panel	Collen Catalog #	Cample Description		
HD 100 LAU panel	17255	Caucasian	<	
	17.50	Caucasiai		
HID 100 CAU panel	1/25/	Caucasian		
HD-100 CAU panel area	17258	Caucasian		
HD 100 CAU panel	17259	Caucasian	*	
HD 100 CAU panel ***	17260	Caucasian		
HD:100 CAU panel 35%	17261	Caucasian		
HD 100 GAU panel men	17262	Caucasian		
HD 100 CAU panel man	17263	Caucasian		
	17264	Caucasian		
033,039	17265	Caucasian	*	
HD 100 CAU panel	17266	Caucasian		
HD:100 CAUrganel 31	17267	Caucasian		
HD 100 GAU panels	17268	Caucasian		
HD 100 CAU panel at a	17269	Caucasian		
HD 100 CAU panels 22	17270	Caucasian	<b>.</b>	
50×53	17271	Caucasian		
	17272	Caucasian	*	
HD 100 CAU panel	17273	Caucasian	*	
	17274	Caucasian		
HID TOP CALL panel 23	17275	Caucasian		
HD 1000At Inanel - 5	17276	Caucasian		
PARTIE OF THE PARTIES	17277	Caucasian	•	
	17978	Carcasian		
	0/5/0	Caucasian		
	6/7/1	Caucasian		
MD tot cAUpanel	1/280	Caucasian		
FILTRUCAU Danellares	1/281	Caucasian		
MD 100 GAU panel	17282	Caucasian		
MD 100 CAU panel 25.	17283	Caucasian		
HD 100 CAU panel.	17284	Caucasian		
HDx100cAU panal	17285	Caucasian		
HOGOLOAU panels	17286	Caucasian		
Professional and	17287	Caucasian		
MD. (00 GAL) panel 328	17288	Caucasian		
MD 100 CAU panelina	17289	Caucasian	P	
FED DO CAU SPIRE	17290	Caucasian		
2016/01/2	17291	Caucasian		
	17292	Caucasian		
	17293	Caucasian		
A CONTRACTOR OF THE PROPERTY O	17294	Caucasian		
	17295	Caucasian		
				TO THE THE PROPERTY OF THE PRO
Omapatrilat Trial Samples, 12 angioedema patients	es 12 angioedema pa	tients	X	WESSERVINE WESSERVINE WITH WESSERVINE WITH WESSERVINE WESSERVINE WESSERVINE WESSERVINE WITH WESSERVINE WESSE

Omapatrilat Trial Samples, 12 angioedema patients

		9.0	100	anoonaa	amely accelerate	Torost Name	PCR Left primer	PCR Left primer (SEQ ID NO:)		PCR Right primer (SEQ ID NO:)
GENE DESCRIPTION	HGNC ID	SNP_ID	EXON.	MEVCOMP	AE100077078	XPNPEP2 X20a	AGTGCTCCTTCCCTTC	297		360
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s2	Intron3	0	AE100p9p10	XPNPEP2_X3a	CAGCCCAGGCATCTTAATCTA	298	TCTCTACTTCCCTCCCTTTGC	361
Aminopaptidase P (membrana-bound)	XPNPFP2	AE10083	Intron15		AE100p57p58	XPNPEP2_X15a	TAGCTGTCTTCCTTCGC	299	ATAGGATGAGGCTCAGCTTGG	362
Aminoparidasa P (membrana-bound)	XPNPEP2	AE10084	Intron15	0	AE100p57p58	XPNPEP2_X15a	TAGCTGTCTTCTTCGC	300	Al Aggal GAGGCI CAGCI I GG	200
Aminorantidasa P (membrana-bound)	XPNPEP2	AE100s5	Intron1	0	AE100p1p2	XPNPEP2_X18	TGATTGAGACCAGCTGTTGTG	301	AACAGAAAAAAGACICGGGC	904
Aminopeotidase P (membrane-bound)	XPNPEP2	AE100s6	Intron7	0	AE100p25p26	XPNPEP2_X7a	CCAGCGTGGGCATACATG	208	GGCCCIGAAAICIGCAIII	368
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s7	Intron7	0	AE100p25p28	XPNPEP2_X7a	CCAGCGTGGGCATACATG	203	GGCCCIGAMAICIGCAITI	287
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s8	Intron10	0	AE100p37p38	XPNPEP2 X10a	CHICCHIIGACCICCAGGAAC	505	CCTGTTTCCTCTGGCTCT	368
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s9	Intron10	٥	AE100p37p38	XPNPEP2 X108	CHICHIGACCICCAGGAAC	908	GGCCCTGAAATCTGCATTT	369
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s10	Intron7	0	AE100p25p26	XPNPEP2 X/8	TO ACTOR OF TO A COURT OF THE	300	CAGCTCTCAGGCCTTTTCATT	370
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s11	Intron13	0	AE100p49p50	XPNPEPZ X138	TANATONOAGEOGIA	S S	CAGCTCTCAGGCCTTTTCATT	371
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s12	Intron13	0	AE100p49p50	XPNPEPZ X138	TANATONOROGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOG	88	CAGCTCTCAGGCCTTTTCATT	372
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s13	Intron13	0	AE100049050	VONDEDO VAS	TGATTGAGACCAGCTGTTGTG	310	AACAGAAAAAGAGACTCGGGC	373
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s14	Exon1	0	AE100D1D2	VONDEDO V18	TGATTGAGACCAGCTGTTGTG	311	AACAGAAAAAGAGACTCGGGC	374
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s15	Exon1	0	AETOOPIDE	VENDEDS Yes	GGCCCATGTCATTAATGAGTAC	312	TCAGGGCTACCTTTGTCCTT	375
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100816	Introns		AE100pSabso	XPNPEP2 X178	CCCTCTTCTTAGGCACCACTC	313	CTGCTGGCATTCCTCACTTAC	376
Aminopeptidase P (memorane-bound)	VONIDEDO	AE100517	Intron17	, ,	AE100065066	XPNPEP2 X178	CCCTCTTCTTAGGCACCACTC	314	CTGCTGGCATTCCTCACTTAC	377
Aminopositions of (membrane hound)	XPNIPEPS	AE100s19	Intron15	0	AE100p57p58	XPNPEP2_X15a	TAGCTGTCTTCTTTCGC	315	ATAGGATGAGGCTCAGCTTGG	378
Aminopepardase P (realingales-bound)	XPNPEP2	AE100s20	Intron21	•	AE100p81p82	XPNPEP2_X21.f18	GGACTATGGTGACAGCTGGAG	316	CAAGAAGCCCTGTGTTCCTG	3/8
Aminopantidase P (membrana-bound)	XPNPEP2	AE100s21	Exon21	0	AE100p81p82	XPNPEP2_X21.f1a	GGACTATGGTGACAGCTGGAG	317	CAAGAAGCCCIGIGIICCIG	200
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s22	Exon21	0	AE100p85p86	XPNPEP2_X21.f2a	GAGGCTCCAGACTCTCCTGTT	318	TASSAATSATSSTATSASTS	380
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s23	Exon21	0	AE100p85p86	XPNPEP2_X21.f2a	GAGGCTCCAGACTCTCCTGTT	319	- AGENATIGATION TO THE TOTAL T	383
Bradykinin Receptor B1	BDKRB1	AE103s1	Exon2	0	AE103p13p14	U48231_X2.f3a	CACTITIGCAAGGAITIGIGGAG	320	CACCACCAGGAAGATGCTG	386
Bradykinin Receptor B1	BDKRB1	AE103s2	Exon2	٥	AE103p5p8	U48231_X2.f18		321	TGGGGGCCAGAATCCTAAAT	385
Bradykinin Receptor B1	BDKRB1	AE103s3	Exon3	٥	AE103p17p18	U48231 X2.14a	AGGACCAAGGICIGGGAACI	322	ATCTCAGTACTTTGGGAGGCC	386
Bradykinin Receptor B1	BDKRB1	AE103s4	Exon1	٥	AE103p1p2	U48231_X18	GCIGCCAGGAGAIIAAAIGA	950	CETEGTETETICATGCAATI	387
Bradykinin Receptor B1	BDKRB1	AE10385	Exon3	0	AE103p25p26	D48231 X2.168	ACTIOCCAGACICAAGGGAIC	305	CTCAGTGTCCAGGGAAATGC	388
Bradykinin Receptor B2	BDKRB2	AE104s1	Intron		AE104033934	BUKHBZ ALITIS	COACTAGGTCCTCACCAGACA	326	CTCAGTGTCCAGGGAAATGC	389
Bradykinin Receptor B2	BOKHBZ	AE10482	Intron 1	-	AE10403054	BUKRR X1.0	GCAGGCAAATACCACTTCAA	327	CCGAGGTTCTCTGGAGAAAA	390
Bradykinin Hecaptor 52	BUNNOZ	ACTORS	Intron.	-	AF104n39n40	RDKRR2 X1.22	GCAGGCAAATACCACTTTCAA	328	CCGAGGTTCTCTGGAGAAAAA	391
Dead-deing December 20	BUKBB	AF104e5	Intron	-	AE104n39n40	BDKRB2 X1.12	GCAGGCAAATACCACTITCAA	329	CCGAGGTTCTCTGGAGAAAAA	392
Bradwkinin Recentor R2	BOKRB2	AE104s6	Intront	-	AE104p39p40	BDKRB2_X1.f2	GCAGGCAAATACCACTTTCAA	330	CCGAGGTTCTCTGGAGAAAA	393
Pradukinin Becentor B2	BDKRB2	AE104s7	Intron2	-	AE104p29p30	BDKRB2_X2a	GCTCTTTCTGGAAGGTCCACT	331	ATACCAACAGCTTCCCCAG11	384
Bradykinin Receptor B2	8DKRB2	AE10488	Exon3	-	AE104p25p26	BDKRB2_X3.f7a	GGTCTCAGCACTGTGATCCTC	335	CAAAGACICAAGIGGGAACGA	080
Bradykinin Receptor B2	BDKRB2	AE104s9	Exon3		AE104p25p26	BDKRB2_X3.f7a	GGTCTCAGCACTGTGATCCTC	333	CAAAGACICAAGIGGGAACGA	307
Bradykinin Recaptor B2	BDKRB2	AE104s10	Exon3	1	AE104p25p28	BDKRB2_X3.f7a	GGTCTCAGCACTGTGAICCIC	48.6	CAAACTCTCTCTCTCAGTA	398
Bradykinin Receptor B2	BDKRB2	AE104s11	Exon3	-	AE104p9p10	BDKHB2_X3.138	TOTACALGCCAGAAGCCTGTT	338	CACTCTCTCTCTCAGTA	388
Bradykinin Receptor B2	BDKRB2	AE104812	Exon3		AETOAPSDIO	BUNHBZ A3.138	TCTACATGCCAGAAGCCTGTT	337	CCACTCTCCTCTGCCTCAGTA	400
Bradykinin Receptor B2	BOKHBZ	AE104813	Exons	- -	AE104p310	ROKRR2 X3.f8a	CCTCCAGCTTCTAGCTCAGGT	338	GCAGAATCAGTATTGGGAGCC	401
Bradykinin Hecepior 62	מסטעסם	AE404e46	3' Flank	-	AF104n3n4	BDKRB2 X3.f1	GCTTAATGCTTGGGTGATGAA	339	CTAGAATCATAGGCGCAGCAG	402
Bradukinin Becantor R2	BDKRB2	AE104817	3' Flank	-	AE104p3p4	BDKRB2_X3.f1	GCTTAATGCTTGGGTGATGAA	340	CTAGAATCATAGGCGCAGCAG	403
Tachvkinin Becentor 1	TACRI	AE106s1	Exon1	-	AE106p23p24	TACR1_X1.f1	CGTGGTCCTCTATGAGCACTT	윮	CATCTCCACTAACACCICGGA	404
Tachvidin Receptor 1	TACR1	AE106s2	Exon2	1	AE106p17p18	TACR1_X28	GGGTATATGTGAGAAATGCTTGC	345	TCATCAGGAAICAAAGGGIIIC	400
Tachykinin Receptor 1	TACR1	AE10683	Intron3	-	AE106p13p14	TACR1 X3a	CTGGGTTCCAAGACACIGAA	-	TOTA ACTOCATOTACAGE	407
Tachykinin Receptor 1	TACRI	AE106s4	Exon5	-	AE106p1p2	TACR1_X5.f1a	CI GCAGGAGGCI AAICTOAGA		TCCAACTGCTCTCACGAAGT	408
Tachykinin Receptor 1	TACR1	AE106s5	Exon5	-	AE106p1p2	TACH1 X5.118	CIGCAGGAGGCIAATCTGAGA		TCCAACTGCTCTTCACGAAGT	409
Tachykinin Receptor 1	TACRI	AE106s6	ExonS		AE106p1p2	TACDA VE MA	ACCONTRACTORACIONALICITATION	247	TAACAAGCTGATGCAGTGGTG	410
Tachykinin Receptor 1	TACRI	AE106s7	Exons	-	AE106557519	CANH YAS	AATACCCTCCATTCCAGCCT	348	TGGAGTGACCTAATGCTCCTG	411
C1 Esterase inhibitor	200	AETOSSI	Introne.	-	AE105017010	CINH X6a	GICTICCCATICTGGGTCCT	349	GGTGGAATACAGATGGAAGGA	412
C1 Esterase immolior		AF105e3	Evon7		AE105n29n30	C1NH X7a	CACTGTTCACCCAGCTGGTAT	350	ACATCITAGGGATCCCCCTTT	413
C1 Estarasa Inhibitor	S S	AE10584	Exon3	0	AE105p9p10	C1NH_X3.f1a	AGATTGCTCATCTGCTGCACT	351	AGTAGTGGGCTGGGTAGGAGA	414
C1 Esterase Inhibitor	CHNH	AE105s5	Exon3	0	AE105p13p14	C1NH_X3.f2a	TTCAGCCACCAAAATAACAGC	352	TGGATTGGTGACTCIIAIGG	415
C1 Esterase Inhibitor	C1NH	AE105s6	Exon8	0	AE105p33p34	C1NH X8.fta	GAACCCAGAGAATTCAGGACA	200	GIGGAIAGCGGACACCIGAG	417
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s1	Exon4	0	AE107p13p14	KIK1 X48	GACTACAGCCACGACCTCATG	35,	GCTCTCAGAAGCCAGTTCAGA	418
Kallikrein 1 (renal/pancreas/salivary)	KLK	AE107s2	Intron4	٥	AE10/p13p14	KIK1 X40	GACTACAGCCACGACCTCATG	356	GCTCTCAGAAGCCAGTTCAGA	419
Kallikrein 1 (renavpancreas/salivary)	KIK	AF10764	Intrond		AE107013014	KLK1 X4a	GACTACAGCCACGACCTCATG	357	GCTCTCAGAAGCCAGTTCAGA	420
Kalikrain 1 (renal/hancress/celivery)	Z Z	AF10785	3' Flank	, 0	AE107p17p18	KLK1 X5a	GCTCCCCAGGCAGACTT	358	CTGCTGGTGACCTCAGACTTC	421
Kallikrein 1 (rana/hancreas/salivary)	KIKI	AE107s6	3' Flank	0	AE107p17p18	KLK1, X5a	GCTCCCAGGCAGAACTT	329	CTGCTGGTGACCTCAGACTIC	422
Nallikieni i (tenakparkieasoaira)	1,1,1	241.41								

HGNC		Ol ANS	EXON	REVCOMP	PCR Amplicon Name	Target_Name	PCR Left primer	PCR Left primer (SEQ ID NO:)	PCR Right primer	PCR Right primer (SEQ ID NO:)
AE103s6 Exo	Exo	Exon3	П	0	AE103p9p10	U48231_X2.f2a	<b>GCCTCTGATCTGGTGTTTGTC</b>	707	CTGTGGTCTTGCTATCCTTCG	740
AE103s7		Exon3		0	AE103p9p10	U48231 X2.f2a	GCTCTGATCTGGTGTTGTC	200	CTGTGGTCTTGCTATCCTTCG	741
AE103s8	T	Exon3	7	0	AE103p9p10	U48231_X2.128	GCCICIGAICIGGIGIIIIGIC	710	AAGAAAGCCAAGCTTCTTGGT	742
AE103S9 Exon3	Exous	xous	1	1	AE103013014	DUYDEN Y2.50	GGCAGGCAGGATTAGTCT	711	AGATCCAGACAGAGAGGGG	743
BUNHB2 AE104S18 Inroni or Exce	Livers	Frond Of E	Ş		AE104pospoo	BOKERO X3-5a	GGCAGGCCAGGAATTAGTCT	712	AGATCCAGACAGAGAGGGG	744
+	Ţ	5'Flank	T	-	AE104n89n90	BDKRB2 x1-3a	CTGGGATTTCTTTGTATGCCA	713	AGAGCCTACAGCCAGTTCACA	745
BDKRB2 AE104s21  5/Flank	Т	5.Flank	T	-	AE104p89p90	BDKRB2_x1-3a	CTGGGATTTCTTTGTATGCCA	714	AGAGCCTACAGCCAGTTCACA	746
AE104s22	Г	5/Flank	1	-	AE104p87p88	BDKRB2_X1-2	ACCTTCGCTCTCCGCTCT	715	AGAAACCTCCGCCATACATCT	747
AE104s23		5'Flank	П	-	AE104p81p82	BDKRB2_X1-18	ACGACCACAGGGAAACTTCTC	31,5	GAGGACGIIIIIGCGGIC	740
AE104824	П	Exon3	┪	-	AE104p65p66	BOKRB2 X3-5a	GGCAGGGCAGGAATTAGTCT	718	AGATOCAGACAGAGAGGAGGG	750
AE104825	Т	Exous	1	†	AE104poppop	DUNNOZ AG-OR	GACCTCCTTGTCCATCAGTGA	719	GGGCTGCTGTGAATTTGTGTA	751
AE104526	T	Exous	1	1	AE104p01p02	BUKRRO X3-3a	TCCCAGTTACGTCTGCGTAAT	720	GCTGAGTGCACAAGTGAGTTG	752
BUNDES ACTUASS/ EXCUS	T	Fyons	т	-	AF104n53n54	BDKRB2 X3-28	GCCACCTTCCAATAAACCATT	721	GGGTGATATGGACAGCAGAAG	753
AE104829	Τ	Exon3	т	-	AE104p53p54	BDKRB2_X3-2a	GCCACCTTCCAATAAACCATT	722	GGGTGATATGGACAGCAGAAG	754
AE109s1	Γ	Intron14	_	-	AE109p25p26	ACE2_x14a	TTAAAAACCCAAAGG	723	TTCTCGTTTTCCAAAAGCCT	199
AE109s2	Г	Intron12	_	_	AE109p29p30	ACE2_x13a	CACCATAGCAGAGAAGAAGCA	724	GCCAAGTCAAGAGAACC	130
ACE2 AE109s3 Intron13		Intron13		1	AE109p29p30	ACE2_x13a	CACCATAGCAGAGAAGGAAGCA	725	GCCAAGICAAAGAGAAACC	/6/
		Intron3	П	1	AE109p69p70	ACE2_x3a	GTAAGGTTGGCAGACATCAGG	726	AAAAAICAIGIICAAAAGGA	750
		Intron2	_	-	AE109p69p70	ACE2_x38	GTAAGGTTGGCAGACATCAGG	121	ΞIE	2007
ACE2 AE109s6 Intron16	П	Intron16	_	-	AE109p17p18	ACE2_x16a		728	CAATTACATCCTCTATTCTTCC	784
AE109s7	П	Exon16		-	AE109p17p18	ACE2_x16a	CTGTGGGATCCTTCTGGAATT	729	TOCOCOLCICATION	769
	П	Intron1		0	AE110p21p22	PI4_X2a	GGACATCTTGATGGGCTCATA	030	TOCOCACTOTICATIVA	783
AE110s2	٦	Exon2	7	٥	AE110p21p22	PI4 X28	GGACAICIIGAIGGGCICAIA	18/	16GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	784
AE110s3	Т	Intron2	_	0	AE110p25p26	PI4_X38	GCC I GGG I ACAAAGGAACCI	702	CCGAGTTCTCTAGGGATTGCT	785
AE110s4	Т	Intron2		0	AE110p25p28	P14 X38	A A S A A C A TOTAL TATAL COOLS	734	CAACAAATTAGTGGGTTGGAGG	788
AE11085	1	Exon1		•	AE110D1/D18	PI4 X1.DB	TACAACCTTTTCCCCTCACA	735	TGAGCTCTGCACAGCACTAGA	787
AE11086		5'Flank	т	٥	AET 10psp6	P14_A1.IZ8	TACAACCITITECCCTCACA	738	TGAGCTCTGCACAGCACTAGA	882
PI4 AET1US/ DEIBUK	-	D'FIBUK	$\tau$	0	AE1100000	Pla X1 fts	ATGETGAGACCCCGACTCTAT	737	TGTTACCCGTACAGACAAGG	769
AE11080	+	5'Elank	-	0	AF110n1n2	PI4 X1f1a	ATGGTGAGGCCCGGACTCTAT	738	TGTTACCCCGTACAGACAAGG	770
D2 AE100c34	t	Intron 1	Т		AF100045046	XPNPEP2 X12a	TITICAAAGCTCCACATCCTG	962	TCGAGTTGTCCTGCTTTCAG	988
AF100s25	Ŧ	Intron13	Г	, c	AE100049050	XPNPEP2 X13a	TAAATGACAGGTCAGGGCTTG	963	CAGCTCTCAGGCCTTTTCATT	686
AE100826		Intron13	Г	0	AE100p49p50	XPNPEP2_X13a	TAAATGACAGGTCAGGGCTTG	964	CAGCTCTCAGGCCTTTTCATT	066
XPNPEP2 AE100827 Intron7	H	Intron7	Г	0	AE100p29p30	XPNPEP2_X8a	GGCCCATGTCATTAATGAGTAC	965	TCAGGGCTACCTTTGTCCTT	991
AE100s28		Exon21	Γ	0	AE100p93p94	XPNPEP2_X21,f4a	GAACTITCCAAAGTGCAGCC	996	ACACATACTCTCAAGCCCACG	992
AE100s29	L	Exon21	Π	0	AE100p93p94	XPNPEP2_X21.f4a	GAACTTTCCAAAGTGCAGCC	967	ACACATACTCTCAAGCCCACG	993
XPNPEP2 AE100s30 Exon6	-	Exone	1	0	AE100p17p18	XPNPEP2_X58	GAGAATCICTITCCAGAGGCC		IGCACGCICICACCIAIACCI	100
AE103s10	+	Exon3	T	0	AE103p25p26	U48231 X2.f8a	ACTICCCAGACICAAGGGAIC		COTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOT	966
AE103811	+	Exons	T		AE103025026	U48231_XZ.ID8	ACTIOCORGACIONAGEGRATO	ļ	CETGETGTTCATGCAATT	266
BUKHBI AE103812 EXONS	+		ſ		AE 103p2p2p	1148231 X2 18a	ACTICCCAGACICAAGGGATC	1	CGTGGTGTGTTCATGCAATT	868
AE103614	+	Fynns	Γ		AF103n25n26	U48231 X2.f6a	ACTTCCCAGACTCAAGGGATC	973	CGTGGTGTTCATGCAATT	666
RDKRR9 AF104830 Exon3	+	Frons	Γ	,	AE104053054	BDKRB2 X3.f2a	GCCACCTTCCAATAAACCATT		GGGTGATATGGACAGCAGAAG	1000
AE104831	ŀ	Exon3	ſ	-	AE104p81p82	BDKRB2_X1.f1a	ACGACCACAGGGAAACTTCTC	975	GAGGACGTTTTGCCGTC	1001
AE104s32	H	Intron1	1	_	AE104p81p82	BDKRB2_X1.f1a	ACGACCACAGGGAAACTTCTC	976	GAGGACGTTTTGCCGTC	1002
H	╀	Intron1	ī	-	AE104p81p82	BDKRB2_X1.f1a	ACGACCACAGGGAAACTTCTC	226	GAGGACGTTTTGCCGTC	1003
AE104834	┞	Exon3	1	-	AE104p73p74	BOKRB2_X3.f7a	TCGCTGTACTCCTTCATGGTC	978	TTTTGTCCTTCCTTGTGAC	1004
AE104935	H	Exon3	آ	-	AE104p73p74	BDKRB2_X3.f7a	TCGCTGTACTCCTTCATGGTC	979	TTTTGTCCTTCCTTGTGAC	1005
L	L	Exon3		-	AE104p73p74	BDKRB2_X3.f7a	TCGCTGTACTCCTTCATGGTC	980	TTTTGTCCTTCCCTIGTGAC	1006
-		Exo	۰	0	AE110p29p30	PI4_X48	ATTICTGGCTCTCGCAGTCTT	981	CCTTTCCAGAGGCAGAACTT	1007
AE110s11	+	Exon	L	0	AE110p1p2	PI4_X1.f18	ATGGTGAGACCCCGACTCTAT	885	TGTTACCCCGTACAGACAAGG	1008
P14 AE110s12 5' Flank	_	5 Fla	ž	0	AE110p1p2	PI4_X1.f1a	ATGGTGAGACCCCGACTCTAT	883	TGTTACCCCGTACAGG	5001
1 AE106\$8	Н	Intro	4	-	AE106p9p10	TACR1_X48	AAGTTAGCTGCAGTCCCCACT	984	GCTTCATCCCATACTGTGCA TATCCACCTCACACACTCTCCC	1010
AE106s9	+	Intro	8	-	AE106p13p14	TACR1 X38	CTGGGTTCCAAAGACACIGAA	000	ALGUAGGIGACAGICICCO	1012
		Intron13	_[	-	AE109p29p30	ACEZ X138	CACCALAGORATICIACAAGCA	800	TGGAATGGAAATTAGAATTGGTT	1013
4	$\dashv$	1 intron6			AE 109p5/p58	AVEZ ADA	CAMANIGUCANITICIANA	400	TOTAL COLOR IN THE PARTY OF THE	

Reverse sequencing primer (SEO ID NO) 486 488 488 488 488 489 489 489 489 489 489	5512 5513 5513 5513 5513 5513 5513 5513	25 25 25 25 25 25 25 25 25 25 25 25 25 2
Ber and a second and a second	.a	200000000000000000000000000000000000000
Fevorate seq panny   Actions   Act	AE(10028)	AE1084 AE10868 AE108502 AE1085
TIGITANTICA MANANTICA MANA	THE ATTACK CARGARITE OF THE AT	TITCAGETTICICIC TITCAGETTICICIC GECATCCETTEATCE GECATCCETTAGET AGATACCTICAGE TO ACATACCTICAGE TO ACATACCTICAGE TO ACATACCTICAGE TO ACATACCTICAGE ACATACTEGAMAN TO ACATACTEGAMAN TO ACATACTEGAMAN
No.)   Reverse	GenTrop   CTTT01   CTTT01   CTTT01   CTTT01   CTT01   CTT01	AAAAAG
Forward a sequencing primer (9EQI DI NO) 422 424 425 426 426 427 426 427 428 428 437 437 438 437 438 444 445 445 446 446 446 446 446 446 446	440 450 450 450 450 450 450 450 450 450	47.1 47.2 47.3 47.3 47.6 47.6 47.6 48.0
esq temp 000171	ET (1992)  ET (1992)  ET (1993)	## (1009.5) ## (1009.5)
	TOTAL CONTROL OF THE	MATABATETT TERANGORATI TERANGO
Ferward seques	CONTGRAMCAC   In a CONTGRAMCAC   In a CONTGRAMCAC   In a CONTGRAMCAC   CONTGRAMCACACAC   CONTGRAMCACACACACACACACACACACACACACACACACACAC	a   GGCTCCAGGAA
Pricomp   Target Name   O   Synker 2 x x x x x x x x x x x x x x x x x x	UM621  ZERIO   UM622  ZERIO   UM62	1   7,007 X 51511   1,007 X 51511   1,007 X 51511   1,007 X 5151
EXON Exon Solution of intronial inte		
HONERS ON THE STATE OF THE STAT	BDVRB1 AE (1004)	12/2021 12/20
Achiocopalidase P (membrane-bound)	Budykinin Neopico 81 Budykinin Neopico 81 Budykinin Neopico 81 Budykinin Neopico 82	Techykinin Receptor 1 Techykinin Receptor 1 Techykinin Receptor 1 Techykinin Receptor 1 Ci Edenses imbblor of Edenses imbblor when I (remit) techniques edes and Edenses imbblor and Edenses imbblor of Edenses imbblor when I (remit) techniques edes and Edenses imbblor and Edens

			HEVE	larger Marne	Forward segmenting primer	forward sed name	Forward sequencing primer (SEC ID NO:)	Heverse sequencing primer	DE DE DATE	Heverse sequencing printer (SECTIO NO.)
Bradykinin Receptor B2	BDKRB2 AE104828	28 Exon3	-	BDKRB2 X3-2a	TTGCTGAGACAGGACAGTCC	AE104p55	785	TATTGCACAACCATCTGTCCC	AE104p56	817
Bradykinin Receptor B2	8DKRB2 AE104s28	⊢	-	BDKRB2 X3-2a	TTGCTGAGACAGGAACAGTCC	AE104p55	786	TATTGCACAACCATCTGTCCC	AE104p56	818
Anglotensin Converting Enzyme 2	۲	Ε	-	ACE2 x148	TTTTGAAAAGAACCACATGGC	AE109p27	787	AGTGGGATCTTTGGAGGAAAA	AE109p28	819
Anglotensin Converting Enzyme 2	H	12 intron12	-	ACE2_x13a	CAGCTGTGTCACAAGTCCTCA	AE109p31	768	ACATCTGGAACCCCTCAAAAG	AE109p32	820
Angiotensin Converting Enzyme 2	H	St Intron13	-	ACE2 x13a	CAGCTGTGTCACAAGTCCTCA	AE109p31	789	ACATCTGGAACCCCTCAAAAG	AE109p32	821
Anglotensin Converting Enzyme 2	ACE2 AE10984	54 Intron3	_	ACE2_x3a	TCATTCATGTCCTTGCCCTTA	AE109p71	290	TCTTCAGCAAATTTCCATTGTT	AE109p72	822
Anglotensin Converting Enzyme 2	┢	H	-	ACE2 x3a	TCATTCATGTCCTTGCCCTTA	AE109p71	781	TCTTCAGCAAAATTTCCATTGTT	AE109p72	823
Anglotensin Converting Enzyme 2	ACE2   AE109s8	96 Intron18	1	ACE2 x18a	GCACACAGGAAGACACACAA	AE109p19	792	COTCCCCATGICTCTATC	AE109p20	824
Anglotensin Converting Enzyme 2	ACE2 AE109s7	-	-	ACE2 x18a	GCACACAGGAAGAACACACAA	AE109p19	793	CCTCCCCCATGTCTCTATC	AE109p20	825
Protease Inhibitor 4	H	┞		Pl4 X2a	GATCTGGAGCGACTGTTTCTG	AE110p23	794	CACACTGATTACCTCTTCCGC	AE110p24	828
Protease Inhibitor 4	r	x2 Exon2	•	PI4 X2a	GATCTGGAGCGACTGTTCTG	AE110p23	795	CACACTGATTACCTCTTCCGC	AE110p24	827
Protease Inhibitor 4	Pl4 AE11083	3 Intron2	۰	P14_X3a	CTTTCAACATCCATTTGTGGG	AE110p27	796	ACTITIGGATGCCTCCAGTTTT	AE110p28	828
Protease Inhibitor 4	Pi4 AE110s4	⊦	0	PI4 X3a	CTTTCAACATCCATTTGTGGG	AE110p27	787	ACTITIGGATGCCTCCAGITIT	AE110p28	829
Protease Inhibitor 4	Pl4 AE11085	55 Exon1		PI4 X1 15a	CTACGCCATGCTTTCCCTG	AE110p19	268	CGGTGGTGTGGATTTAGCATA	AE110p20	830
Protease Inhibitor 4	PI4 AE11088	8 S'Flank	0	PI4 X1 f2a	TTGGGGGAGAACTGGAGTAT	AE110p7	799	CCAACAGAGCAGGAAATGAAG	AE110p8	831
Professe inhibitor 4	H	7 5'Flank	0	Pl4 X1,12a	TTGGGGGAGAAACTGGAGTAT	AE110p7	800	CCAACAGAGCAGGAAATGAAG	AE110p8	832
Protease Inhibitor 4	t	H	٥	Pl4 X1.fta	AAAATTAGCTGGGTGTGGCT	AE110p3	801	TAAGTGACCTGCCCAAAGTTG	AE110p4	833
Protease Inhibitor 4	Pi4 AE11089	┝	٥	P14 X1 f18	AAAATTAGCTGGGTGTGGCT	AE11003	802	TAAGTGACCTGCCCAAAGTTG	AE110p4	834
(punoq-e	XPNPEP2   AE100624	L	0	XPNPEP2 X12a	ATCTCCATCATCTTGGAGCCT	AE100p47	1014	ACCCAAGAACCTGTCACTCCT	AE100p48	1040
-	•	L	0		AGTTGAGAGGTAGAGGCAGCC	AE100p51	1015	GCAACTCCCTACTCCACACTG	AE100p52	1041
Aminopeptidase P (membrane-bound)	XPNPEP2 AE100826	┡	0	XPNPEP2 X13a	AGTTGAGAGGTAGAGGCAGCC	AE100p51	1016	GCAACTCCCTACTCCACACTG	AE100p52	1042
-	XPNPEP2   AE100827	H	0	XPNPEP2 X8a	AGGETTTCGCTGCTTTTAAG	AE100p31	1017	CTTACCCTTCTTGGTTCCCAC	AE100p32	1043
┰	1-	┡		XPNPEP2 X21 f4a	CAATGCTGTTAAATCCTCCCA	AE100p85	1018	CTCACCCTCTCTTCTTCCTCC	AE100p96	1044
┢	XPNPEP2 AE100829	╙		XPNPEP2 X21.14a	CAATGCTGTTAAATCCTCCCA	AE100p85	1019	CTCACCCTCTCTTCTTCCTCC	AE100p96	1045
Aminopeptidase P (membrane-bound)	XPNPEP2 AE100830	30 Exon6	-	XPNPEP2 X5a	ACATCCATCAGCTAATGCCAC	AE100p19	1020	GAACCTAGTCCAGGTCCCAAG	AE100p20	1046
┰	-	┡	۰	U48231 X2 16a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1021	TGGTGTGTTCATGCAATTTCT	AE103p28	1047
Bradykinin Receptor B1	BDKRB1 AE103s11	L	0	U48231 X2 16a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1022	TGGTGTGTTCATGCAATTTCT	AE103p28	1048
Bradykinin Receptor B1	BDKRB1 AE103s12	L	•	U48231_X2 f6a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1023	TGGTGTGTTCATGCAATTTCT	AE103p28	1049
Bradykinin Receptor B1	BDKRB1 AE103s13	13 Exon3	0	U48231 X2 f8a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1024	TGGTGTGTTCATGCAATTTCT	AE103p28	1050
Bradykinin Receptor B1	Т	ļ.,	•	U48231 X2.f8a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1025	Tegrafattcatecaatttct	AE103p28	1051
Bradykinin Receptor B2	١	<b>!</b>	-	BOKRB2 X3.12s	TTGCTGAGACAGGAACAGTCC	AE104p55	1026	TATTECACAACCATCTGTCCC	AE104p58	1052
Bradykinin Receptor B2	BDKRB2 AE104831	L	-	BDKRB2_X1.f1s	CTCTGTGCTGGGACAGTTTGT	AE104p83	1027	GAGCTACGCAAACATGGAAAT	AE104p84	1053
Bradykinin Receptor B2	┪	┡	-	BDKRB2 X1.f1s	CTCTGTGCTGGGACAGTTTGT	AE104p83	1028	GAGCTACGCAAACATGGAAAT	AE104p84	1054
Bradykinin Receptor B2	BUKRB2 AE104833	33 Intron1	-	BDKRB2 X1.11a	CTCTGTGCTGGGACAGTTTGT	AE104p83	1029	GAGCTACGCAAACATGGAAAT	AE104p84	1055
Bradykinin Receptor B2	1	L	-	BDKRB2 X3 f7a	CCCAGATCACCAAGCTGTAGA	AE104p75	1030	CTITICCACTITCTITCAGCG	AE104p76	1058
Bradykinin Receptor B2	Г	35 Exon3	-	BOKRB2 X3 17a	CCCAGATCACCAAGCTGTAGA	AE104p76	1601	CTITICCACTITICTITICAGGG	AE104p76	1057
Bradykinin Receptor B2	г	L	-	BDKRB2 X3 17a	CCCAGATCACCAAGCTGTAGA	AE104p76	1032	CTTTCCACTTCTTCAGCG	AE104p76	1058
Protease inhibitor 4	Т	Ļ	-	P14 X48	TCTCTTGCTGGCTTGGAGATA	AE110p31	1033	CAGGGTGTGGAATGTCCAG	AE110p32	1059
Protease inhibitor 4	PI4 AE11081	11 Exon1	-	PI4_X1.11s	AAAATTAGCTGGGTGTGGCT	AE110p3	1034	TAAGTGACCTGCCCAAAGTTG	· AE110p4	1080
Protease inhibitor 4	Pl4 AE110s12	12 5' Flank	-	PI4_X1.f1a	AAAAATTAGCTGGGTGTGGCT	AE110p3	1035	TAAGTGACCTGCCCAAAGTTG	AE110p4	1081
Tachvidnin Receptor 1	TACR1 AE10888	98 Intron4	-	TACR1 X4a	TGTCCTCTTGTCTCACAGCT	AE106011	1036	CTCACCTGTCTCACCCTCTTG	AE108p12	1062
Tachyldnin Receptor 1	t	L	-	TACR1 X3a	corococococoratiaci	AE106p15	1037	GTAGCTGCCAAACCTTGACTG	AE108p18	1063
Angiotensin Converting Enzyme 2	┢	Γ	3	ACE2 X13a	CAGCTGTCACAAGTCCTCA	AE109p31	1038	ACATCTGGAACCCCTCAAAAG	AE109p32	1064
	t	ł			***************************************	47,00	9997	**************************************		

AE100s1 AE100s10 AE100s11 AE100s12 AE100s13 AE100s14 AE100s15 AE100s17 AE100s18 AE100s18 AE100s2 AE100s2 AE100s2 AE100s2	TATCATTINGTGCCCTATGACCG  AAACTTCATCATCAGAGGAAAGAAAAAAAAAA	1066		( ) ( ) ( ) ( ) ( ) ( ) ( ) ( )		
210 211 211 212 213 214 215 216 216 218 319 319	AAACTTCATCATCAGAGGTACCAAAG ATAGAATGACTTCCTCCAGAGGA	0007	CAGGGTCAGGGAGAAGGC	1154	CCTCATCGATGTCNGCCTGCTGTCTCC	1242
2112 212 213 214 214 215 216 217 218 218 220	ATAGAATGACTTCCTCCAGAGGA	1067	GAGGACATTTGATTCAGACTCCTC	1155	GTGGTTTGCAAACCTTAGCATGCAC	1243
312 314 314 315 316 317 318 318 318 319 319	で用いていて用いないないないの日	1068	CAGCCTAACCCTGYACTGGG	1156	TGGAAGCCCAGNCCCCAGAGGT	1244
813 815 815 816 817 818 819 82 82 82	100000000000000000000000000000000000000	1069	GAAGGCAGCCTAACCCTG	1157	AGCCCAGGCCCCAGAGGTYCTCCCA	1245
314 315 316 317 317 318 32 32 32	ATAGAATGACTTCCTCCAGAGGGA	1070	GCTGAGAAGGGGAGAATGTT	1158	AATGTTGAGAANGNCAGCCTAACCCTG	1246
\$15 \$16 \$17 \$17 \$19 \$20	N/A	N/A	N/A	N/A	N/A	N/A
\$16 \$17 \$18 \$19 \$20 \$20	ACCCTCTGTCTGCTCGAG	1071	GATGGAGGGACAAGGGAG	1159	CCCGGSCTCTTCCTTCANGCNTTTCCT	1247
\$17 \$18 \$19 \$20 \$20	AAAGAAGGAAGGAAAGGAA	1072	GTGTAGGAATAGAAGAAGGGGTTATAGG	1160	AGAAAAGCTTGNCTCAGGCAGATCAGC	1248
\$18 \$19 \$20 \$20	N/A	N/A	N/A	N/A	N/A	N/A
\$19 \$20	AACACAGCAAGACCCCTCTCA	1073	GATCCCAGAGCATCTCTATGAGC	1161	TACCTAAATAATAAAAAGCCAG	1249
\$2 \$20	N/A	N/A	N/A	N/A	N/A	N/A
\$20	ATAGAATTTGCAGGGCAGGG	1074	GTATCTTTGCAGTTCAACTCCCC	1162	GCAACAAGTCTCCTTTNCAGAACAGTC	1250
121	TACCACAACAGGGGACTGG	1075	GATTCAGGTACTGGAGCTGCG	1163	AGACTTCACCTCTTGGCANCTTGGCTT	1251
	N/A	N/A	N/A	N/A	N/A	N/A
AE100s22	N/A	N/A	N/A	N/A	N/A	N/A
AE100s23	TTTGCCTAAGGACACACAAATTT	1076	GAGGTGGGCTCAGGGACT	1164	CTGCATGTTGCTGAAGGGTGAAAGA	1252
AE100s24	CGCTATCTGATCTCCATCT	1077	CCGCACCTGGAGTTGGGG	1165	TINGAGCCTGTGGCTNCAACCAGACCT	1253
AE100s25	N/A	N/A	N/A	N/A	N/A	N/A
AE100s26	N/A	N/A	N/A	N/A	N/A	N/A
AE100s27	ACAAGTAAGAGTTTGTTTGAGGAAAGG	1078	GAGCCCCAAAAAGTGTAAGTGA	1166	TTACCCTANGGCTGACCTNCCAGGAAC	1254
AE100s28	N/A	N/A	N/A	N/A	N/A	N/A
AE100s29	N/A	N/A	N/A	N/A	N/A	N/A
AE100s3	N/A	N/Ą	N/A	N/A	N/A	N/A
AE100s30	TATCTTTCAGTTGGCACCA	1079	CAATGGACAAGAGGGG	1167	TCACCTGGCTCCTCACCGAGATTCC	1255
AE100s4	TCCCTGCTGCTTCCCCGG	1080	AATATTTGTGCACTGATTTACCAGAATAG	1168	TATTTCAGNCCACTGACANGGCCTCAG	1256
AE100s5	N/A	N/A	N/A	N/A	N/A	N/A
AE100s6	TGTGTGTGCATGAGTGTG	1081	CTTTGTCATTTCCATACCTGTGAAA	1169	ACCTTCATAGAGGGTATAATAAAG	1257
AE100s7	ATCCAGTAATGGCAAAGCCAG	1082	GTCAGCCTTAGGGTAACAGTTTG	1170	AAGAGTTTGTTTGAGGAAAGGGTTT	1258
AE100s8	GCAAATCTCACGTCTGCTG	1083	CAGGTCTGGGGCCACAGTA	1171	GTAAAGGAGGTCTCNATNGCACAGGGG	1259
AE100s9	AAAACTAGGAAAGACAGAAAGCACAC	1084	TTTCAGAGGACTGGCAGGAG	1172	CACAGAGTAGAGAGNATTGCCACGAAA	1260
AE103s1	AACTTCTTTGCCTTCACTAACAGCT	1085	GATGAAGATATTGGAGCAAGACTTTTAG	1173	CCAGTAATTTATGTCTTTGTGGGCC	1261
AE103s10	N/A	N/A	N/A	N/A	N/A	N/A
AE103s11	TGGACTTGATGATGTTACCAAATT	1086	GACTCTGAGCCTCCTGCCTC	1174	ATCCTGAATTATCCAAGTGGGCCCT	1262
AE103s12	N/A	N/A	W/A	N/A	N/A	N/A
AE103s13	CCACCGAGTTTCTGGTAATTTG	1087	CTTTGAATAGACAAATGGAAGTGTARTAAGA	1175	CAGCAGGAACAAATAACAAGTATC	1263
AE103s14	TGTCATAGCAGCAGGAA	1088	CCTGGÇAGTTAGÇCTAGAAAGC	1176	ACAAGTATCRGGTAATGNCCTCTCTTA	1264
AE103s2	TGACAATGCTCCAGAAGCC	1089	CAACAGGACAAAAAGGTTCCC	1177	CTGGGACCTGCTGNACAGAGTGCTGCC	1265
AE103s3	ACTTTTCTGGCGGAATTAAAACA	1090	ACCCCCAATCTACGGGA	1178	TGAACCAANANGCTTGGCTTTCTTATC	1266
AE103s4	N/A	N/A	N/A	N/A	N/A	N/A
AE103s5	N/A	N/A	N/A	N/A	N/A	N/A
AE103s6	TTCTGGGCAGAGAATATCTGGA	1091	CCACCAGGAAGATGCTGATG	1179	GAGCCCTCCTGCCGTGTCATCAA	1267
AE103s7	N/A	N/A	N/A	N/A	N/A	N/A
AE103s8	ATCTGAACATCACCGCCT	1092	GTAGTTGAAGAAGACGATCGC	1180	AGATCTGAACATCACCGCCTGCATC	1268
AE103s9	N/A	N/A	N/A	N/A	N/A	N/A
AE104s1 G	GAGAGCAATAAATGTCTGTTTTTTTGATAA	1093	CTCACCTGTGCTGTTGTG	1181	CACTGGGCAAATCNGCNGGGCTCCCCC	1269
_	GGTTGGGGCCTCAGGGTG	1094	GTGGCGGTGTGAAGCACC	1182	GTNGGAATGACAGGTNGAAGGGAGCCA	1270

GI_GN8	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:)	ORCHID_SNPIT	ORCHID_SNPIT (SEQ ID NO:)
AE104s11	TTGGATGTGAAATGCTTCCTG	1095	GCCCTATGCATGTGTGTG	1183	TTACAACATAACAGCNCATTGAGTCTT	1271
AE104s12	ATTTTCTCGTTTGGATGTGAATG	1096	CGGCCCTATGCATGGTGTA	1184	TAACAGCTCATTGAGTCTTKCACAG	1272
AE104s13	GCCATTGCGGCAGAGCTC	1097	AAAAAAGAGGCTGTGTTTTTGTCA	1185	GGCCAGTCATTCAGCACCAGAGCAC	1273
AE104s14	AAGTGAATGAGTGCTGCCCT	1098	AAGGTGGCCCAGTATGAGC	1186	CCCTAGAAGAGTGTGAAAAGGAATG	1274
AE104s16	GATGCATGGATGGAGG	1099	CAGTGATGGGGAATTCATTATCC	1187	ATTCCTTCACTCATNTATNAAACAAAA	1275
AE104s17	GATGGAACAGATGAAGGAGAGG	1100	CATAAATGCCCCTCCTCCAT	1188	TACGTTGAGCGATGAGCCCCAGGTT	1276
AE104s18	AGAAGAAGATGGTTAGATGGCA	1101	CATTGAGTCAGGGACTCAGCA	1189	ACAGGGGCTGGGGATNGCNAAATACAC	1277
AE104819	TAACTAGTGAACTGAGGAATCCCTTT	1102	CACTCTGAGTCCAAATGTTCTCTC	1190	GTGGTGGCACGGAGTCCTCAC	1278
AE104s2	GAGAGCAATAAATGTCTGTTTTTTGATAA	1103	CTCACCTGTGCTGTG	1191	GTCAGGGAGGGCNCACCTGGGCGCGG	1279
AE104s20	TTTACACTCCCAGGGCTGAG	1104	CTCTTCCCCAGATCCACTGG	1192	TTTTTGNAGCCTTAAAACCCTTCCTTC	1280
AE104s21	GGATTTCTTTGTAYGCCACGTAC	1105	CATACATCTCCGAAGAAACGG	1193	GCAGAAGCTGTCCTGTTTCCTGGGT	1281
AE104822	N/A	N/A	N/A	N/A	N/A	N/A
AE104s23	AGAGCTGGAGTGGCGGCG	1106	GCAGGAGTGCAGAGCTCAG	1194	GAAGTGCCCAGGAGGCTGNTGACATCA	1282
AE104s24	N/A	N/A	N/A	N/A	N/A	N/A
AE104825	N/A	N/A	N/A	N/A	N/A	N/A
AE104826	TGAATAGATTAAAGAAACCCAGGG	1107	Gricicarcciaeccc	1195	CATTGCACCAAANCTGGATGGC	1283
AE104s27	TCGACCGTCTCGTCGAAC	1108	GAAAGAAGGAGCCATCTCCA	1196	GCTTTCNGGTGGTGNCAGTGCCCAGTC	1284
AE104828	N/A	N/A	N/A	N/A	N/A	N/A
AE104829	N/A	N/A	N/A	N/A	N/A	N/A
AE10483	TTTGCAAGGGAGAATC	1109	CAACCCTGCACTCCAAGC	1197	GAGCGAAGGCTGGCTGAGGTCATG	1285
AE104830	N/A	N/A	N/A	N/A	N/A	N/A
AE104s31	N/A	N/A	N/A	N/A	N/A	N/A
AE104832	N/A	N/A	N/A	N/A	N/A	N/A
AE104833	TAGGGATACAATGGCTAGGAGCT	1110	GTTTGGGACCCCATGTTCTAT	1198	ACCITITGCITGATITITCACTGIA	1286
AE104834	ACACTGGTGCTTCACACCG	1111	GTACATGTGAGGCATCWTTACGC	1199	GGCTCCCAATACTGATTCTGCTCCA	1287
AE104835	N/A	N/A	N/A	N/A	N/A	N/A
AE104836	CCCTTCTGCTGTCCATATCA	1112	CATCTTGAAGGAACTCAAAGACTCA	1200	ACCCACAGCACCCTGCTNGACCGTCTC	1288
AE10484	AGTGAGGCTTGGAGTGCA	1113	CTTTGGATGAAAAGAGGAAGCA	1201	AGGGTTGCAGGGAGANCTGGGATGAGG	1289
AE104s5	TGCAGGGTTGCAGGGAGA	1114	CAAGAGAGGCGTCTTTGGAT	1202	GCTGGGATGANGYCTGGGGTGCTGCCT	1290
AE104s6	GGCTCACAACTGTGGAATGTC	1115	CAAAGAGCCCTGCCCGA	1203	GTTCTCTGGAGAAAAACTGTGCTG	1291
AE104s7	AACTGTGGCCCAGAGGGT	1116	AACCCCTTACCCACCAGC	1204	CCCCTCTCCAAGTCTNTGTCCCACAA	1292
AE104s8	ATGTACGTAGCACCCTTTGCTTT	1117	GGAGACCAAGGTTCCAGCTC	1205	GAAGAGGAACTGAGGCAGGGACAG	1293
AE10489	TATTTCTAGACCTCAGTGTCTTTTTCCTTATAG	1118	GAAGTCGTTGTGAGGGTTAAAGG	1206	AAGGGTGCTACGTANATNTGAGGCATC	1294
AE105s1	GAGAGCTCTGAAGGGGG	1119	AGGITCITICACCTGCTGCA	1207	CCCAGCGCTGGGGAAAGAAAGGACA	1295
AE10582	ATTGTGACAGAGGGTGGGG	1120	CAAACTCAGATTGTGGGAGAGC	1208	GAGATGCGGTAGGAAGACTGTTAAG	1296
AE10583	N/A	N/A	N/A	N/A	N/A	N/A
AE10584	GCGAAGGGAAGGTCGCAA	1121	TTGAGTTGGTTGTCGGCAA	1209	AAGCTGGAANCCTCNAGGATGGGTTCA	1297
AE10585	TGTTGGGGGATGCTTTGG	1122	GATGCTGAATGGGGAAAAGG	1210	AAGCTCTACCACGCCTTCTCAG	1298
AE105s6	ATCTCTGTGGCCCGCACC	1123	CATATACTCGCCCCATGAAGAC	1211	GGAACTTGTNCTNCTGGTCCCAGAGCA	1299
AE106s1	TATCAAAGGCCACAGGCCG	1124	CACAACGAATGGTACTACGGC	1212	TACTGGCGAAGACAGCGGCGATGGG	1300
AE106s2	ATGGTCTCTGTGGTTGAGTAGTAGC	1125	CATCATACATCCCCTCCAGC	1213	CCAGCAGGAGAGCCAGGACCCA	1301
AE10683	ATACCTGGGGATATTTTGTGC	1126	CTACCACGAGCAAGTCTCTG	1214	CCAAGCGCAAGGTGAGCAGGGG	1302
AE10684	TGCAGAATTCATCCTGAAATGA	1127	CTGTKTGACTCAAACCAAATCACT	1215	AGGTCGGACCANCTTTTCCCAA	1303
AE10685	AAAAGCTGGTCCGACCTTTTATT	1128	TCAAAAATCTCAATTCTTCCCTATCT	1216	TCCCTATCTTTGCNACNCTNATGCTGT	1304
AE106s6	TTTGAGTCAMACAGCATGAGG	1129	CATGGAAATTCCCTTCATCTG	1217	ACCCATACTGACCCTTTTNGCAAGTCC	1305
AE106s7	ATGGTCTTGGAGTCACTTCGTG	1130	CCCACGAGGAGGCCAG	1218	AGAGCAGTINGAGGTCAGGTNCAGGGA	1306

		ORCHID_LEFT (SEQ		ORCHID_RIGHT		ORCHID_SNPIT (SEQ
SNP_ID	ORCHID_LEFT	ID NO:)	ORCHID_RIGHT	(SEQ ID NO:)	ORCHID_SNPIT	ID NO:)
AE10688	N/A	N/A	N/A	N/A	N/A	N/A
AE10689	N/A	N/A	N/A	N/A	N/A	N/A
AE107s1	GITCGTAGTCTCATTTCCAGATGATC	1131	ACACAGCATGAAGTCTGTCAC	1219	CAAAATCCTGCCTAATGATGAGTGC	1307
AE107s2	AGCATCGAACCAGAGAATTGTATG	1132	CTTCCCTGGCCCTTTCTC	1220	TCCCTTGNACRCAGGAGTCCCCATCCC	1308
AE107s3	CCTGCTGATACCATCACAGATG	1133	CATACAATTCTCTGGTTCGATGC	1221	GCTGTGAGNTCGNGGAGTTGCCCACC	1309
AE107s4	ATCGAACCAGAGAATTGTATGTGG	1134	GGGAGAAAAGGGCTGCA	1222	AAGGCRGGGATGGGGACTCCTG	1310
AE107s5	ACCTGGACCCACTCGGCT	1135	CCTTTCCCCACCTGCTGG	1223	TGNGGCCACCCCAGCTGTGTCA	1311
AE107s6	CCAGTAAATCAAATGTGCATCC	1136	CAGCCTCAGCCGAGTGGG	1224	ATGTGTCACGTTCTGCCATCACC	1312
AE109s1	AATAGCTTATCCAATAAGGAATAGGTTACTTT	1137	GAATTGATTTTTTGAGTGCACAGTC	1225	ATCTGGAACTTATAGTNTTGAAAAGAA	1313
AE109s2	GGGGGTTCAGGGCCTTTT	1138	GCAAATTTAGCCAAGTCAAAGAGA	1226	GAGGGGTTCCAGANGTACNTATATTTA	1314
AE109s3	TGGGGCCAAAGGAGACTAG	1139	GCTGAAAGACCAGAACAAGAATTC	1227	AAGTAGACAAGGAATGGGTGTGAAA	1315
AE109s4	GTGTTGAAACACACATATCTGCAAT	1140	TGGAAAGTTTGTAACCCAGATAATC	1228	TCATAATCACNANTNAAANTTAGTAGC	1316
AE109s5	GTGTTCAACTGCAAATTAAAGATAATAAACA	1141	ACATGCCAAAGAAGTAAATTGCTG	1229	GAAATTTTGCTGAAGAGAATGCTAA	1317
AE109s6	AACTCAAATCAAGATTATTCCCCTG	1142	GTTACCAAATACAACAACAATAACCAGTATT	1230	CACATGTAAATGACTCAGAATAATG	1318
AE109s7	CCCTCACCCTTAGATGAAAAA	1143	TTTGAAACCAAGAATCTCCTTTAATTT	1231	TTCAGTTCTAGGAATNATATCAGACAC	1319
AE109s8	N/A	N/A	N/A	N/A	N/A	N/A
AE109s9	AGGCTCACTCAAAAAGGCAATT	1144	TGCCTCCCTGCTCATTTG	1232	CTTGGTAANAAGCCCCATNAATTCTTC	1320
AE110s1	N/A	N/A	N/A	N/A	N/A	N/A
AE110s10	CACCTTGGACGTGATGAG	1145	ATGTGGCGATTGGTCTGG	1233	GGNTGGCACCGAGGNTGCAGCAGCCAC	1321
AE110s11	CACCTCCTGCACTCTCA	1146	CATGGTGTCATTCAGGAATTTTG	1234	AACCTCNCCGGNCATGGGCTGGAAACA	1322
AE110s12	AGATTTGGGGGAGAAACTGG	1147	CAGTAGAACTGGTCTTTGTATTGTTACC	1235	TNTCTTGGACAGATGTTNATTATGAAA	1323
AE110s2	CTGTACCTTCTTTCATCTTCCTT	1148	GCAGCATCATGGGCACCC	1236	CCGGACTGNTGTGTTCTCATCAACATA	1324
AE110s3	AAGGAGGCTCTGCCCAG	1149	GATGCAACTCTAGCTTCTTGTAAAATT	1237	GATCCTGGCTTGTTCANTANTCTAATG	1325
AE110s4	N/A	N/A	N/A	N/A	N/A	N/A
AE110s5	CTTATCAACGACCACGTCAAGAA	1150	GATTTAGCATATACCAATGATCTGACTCT	1238	GAGGGAAGATTGTGGATTTGGTCAG	1326
AE110s6	GTCAAACTAAATGGCTGAAAGTGG	1151	TTTCAGATGAGTTGATTTCATTAGTGC	1239	AGACCCTAAAATAAACTCTGAGGAT	1327
AE110s7	AGGGTCAAACTAAATGGCTGAAA	1152	CACTTGTCTTTCAGATGAGTTGATTTC	1240	TAAACCATATAAAGCACTCCACAGA	1328
AE110s8	AGAAACTGGAGTATCCTTTCTTGGA	1153	CTGTAGAGGTCAGTAGAACTGGTCTTTG	1241	TATGAAACGNGTACCANTTCTATCCCC	1329
AE110s9	N/A	N/A	N/A	N/A	W/A	N/A

£ 6	LABY: DKU	GBS LEFT (SEQ	CBS RICHT	GBS_RIGHT (SEQ ID NO:)
200	# 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1220		1461
AETOOST	TIGITAAAACGACGAGTAGTTICCTCCTCCTCCTCCTCTCT	1330	CAGGAAACAGCIAIGACCAGAAGCICIGGGGICIC	
AE100s10		1331	CAGGAAACAGCTATGACCCACCAGGCAAGCAAATC	
AE100s11	TGTAAAACGACGGCCAGTTTCTGGGCTTTACCCTCTCTC	1332	CAGGAAACAGCTATGACCAGGTCTGAGCAGAGACA	1453
AE100s12	TGTAAAACGACGAGTTTCTGGGCTTTACCCTCTCTC	1333	CAGGAAACAGCTATGACCAGGTCTGAGCAGAGACA	1454
AE100s13	TGTAAAACGACGGCCAGTCCAGGTGCAGGATTAACAGAC	1334	CAGGAAACAGCTATGACCAGGTCTGAGCAGAGACA	1455
AE100s14	TGTAAAACGACGACCAGTACTAGGAACTTGCACAGTCCG	1335	CAGGAAACAGCTATGACCATGCACATACCACAGAG	1456
AE100s15	TGTAAAACGACGACCAGTCCTCACACCCTATCCTACACG	1336	CAGGAAACAGCTATGACCATGCACATACCACAGAG	1457
AE100s16	TGTAAAACGACGGCCAGTCAGTGAGATCTTGCCACTGC	1337	CAGGAAACAGCTATGACCCAAGCTAAGGAAAAGCC	1458
AE100s17	TGTAAAACGACGCCAGTCAGGCAGACAATGATGTGATG	1338	CAGGAAACAGCTATGACCTGTGCTCCTCTGAAGTC	1459
AE100s18	TGTAAAACGACGGCCAGTTATCCAGGTATGGTGGCATGT	1339	CAGGAAACAGCTATGACCATAGCGATGTTGTTGGA	1460
AE100s19	TGTAAAACGACGCCAGTCAGAGGAAGCACGTGATG	1340	CAGGAAACAGCTATGACCACTGGTTTCTGAAACCC	1461
AE100s2	TGTAAAACGACGCCAGTTGTAAAGCCCTTTGCAGAAGT	1341	CAGGAAACAGCTATGACCCTTGTCAGCTACAAGCC	
AE100s20	TGTAAAACGACGCCAGTCTCTGAAAAGCCCCAGAGAAT	1342	CAGGAAACAGCTATGACCCTGTTGAAGCCACTCGA	1463
AE100s21	TGTAAAACGACGGCCAGTGAGGCTCCAGACTCTCCTGTT	1343	CAGGAAACAGCTATGACCGGAGCAGCTGTAGCAGT	1464
AE100s22	TGTAAAACGACGACCAGTCATTGCCTAGAAACCTTTGCA	1344	CAGGAAACAGCTATGACCATTGCTCTTGGGGTT	1465
AE100s23	AE100s23 TGTAAAACGACGGCCAGTAGCCACAGCTACAATGCTGTT	1345	CAGGAAACAGCTATGACCAAAACCCAGAGGCAAGT	1466
AE100824	AE100s24 TGTAAAACGACGGCCAGTCTGCCGTCAACACAGAACTCT	1346	CAGGAAACAGCTATGACCGAACTTGTCCACGATCT	1467
AE100s25	AE100s25 TGTAAAACGACGGCCAGTAGAAGAACAGTTCTCCTCCGG	1347	CAGGAAACAGCTATGACCCCATGTGAACTCGTGAG	1468
AE100826	AE100s26 TGTAAAACGACGCCAGTCATGCCTTGCCTTGTACTTTC	1348	CAGGAAACAGCTATGACCGGCAACTCCCTACTCCA	1469
AE100s27	TGTAAAACGACGCCAGTATGGAACACAGAGGGGTTAGG	1349	CAGGAAACAGCTATGACCGTCTGCAAATCCACAT	1470
AE100s28	AE100s28 TGTAAAACGACGGCCAGTGGGTTGTATACCACACCCTGG	1350	CAGGAAACAGCTATGACCACAGCCAAATTCCTATG	1471
AE100s29	AE100s29 TGTAAAACGACGGCCAGTCGAGATAGGAAAGCCAGCTAG	1351	CAGGAAACAGCTATGACCGTTCTCCAACCTCTGGT	1472
AE100s3	TGTAAAACGACGACCAGTCACTTGTGGAAAGCACACAGA	1352	CAGGAAACAGCTATGACCTGTCAGTGGCCTGAAAT	1473
AE100s30	AE100s30 TGTAAAACGACGGCCAGTAGGAAATTTGAGGCCATCACT	1353	CAGGAAACAGCTATGACCCCTCCTTCTACCAAGGT	1474
AE100s4	TGTAAAACGACCAGTAGCAGTCAAGATCCCTTCCAT	1354	CAGGAAACAGCTATGACCGTTTCCTGAACACCTCT	1475
AE100s5	TGTAAAACGACGAGTGAAAGAGCCCTCCTCTCTC	1355	CAGGAAACAGCTATGACCTTGCAATGCGGTAGTCT	1476
AE100s6	TGTAAAACGACGCCAGTCAAGGTGGACAGTCTTCGGTA	1356	CAGGAAACAGCTATGACCCTGCTGGCATTCCTCAC	1477
AE100s7	TGTAAAACGACGCCAGTTCCTCATAGCAGCCCTATTGA	1357	CAGGAAACAGCTATGACCGGACGCCAGATACTTTC	1478
AE100s8	TGTAAAACGACGGCCAGTATCCGAAGACAGGGAGTTCAT	1358	CAGGAAACAGCTATGACCCTGTTCTTCACTGCCTT	1479
AE10089	TGTAAAACGACGCCAGTATCCGAAGACAGGGAGTTCAT	1359	CAGGAAACAGCTATGACCTGGGGAGTAGGTGTCTG	1480
AE103s1		1360	CAGGAAACAGCTATGACCTCAATGCTGTTTTAATT	1481
AE103s10	TGTAAAACGACGCCAGTCGTCCCAGATCTGAACATCAC	1361	CAGGAAACAGCTATGACCGACTGCTTGCACCTGGA	1482
AE103s11	TGTAAAACGACGCCAGTGAACCAAGAAGCTTGGCTTTC	1362	CAGGAAACAGCTATGACCCTAAATCTGTTTCCCTG	1483
AE103s12	TGTAAAACGACGGCCAGTAACTTCCCAGACTCAAGGGAT	1363	CAGGAAACAGCTATGACCTCCCTGTATTCCTGGCA	
AE103s13	TGTAAAACGACGACCAGTCAAGTGATCCTCCACTTTGGT	1364	CAGGAAACAGCTATGACCTGGTGTGTTCATGCAAT	
AE103s14		1365	CAGGAAACAGCTATGACCTGGTGTGTTCATGCAAT	
AE10382		1366	CAGGAAACAGCTATGACCGATATTCTCTGCCCAGA	
AE10383		1367	CAGGAAACAGCTATGACCCTGAATTCCTCTGGCCT	1488
AE10384		1368	CAGGAAACAGCTATGACCAAGGCAGATGGATCAGA	1489
AE103s5		1369	CAGGAAACAGCTATGACCTCCCTGTATTCCTGGCA	
AE103s6		1370	CAGGAAACAGCTATGACCAGTGGTAGGAGGAAACC	1491
AE103s7		1371	CAGGAAACAGCTATGACCAGTGGTAGGAGGAAACC	1492
AE10388		1372	CAGGAAACAGCTATGACCCTGTGGTCTTGCTATCC	1493
AE103s9		1373	CAGGAAACAGCTATGACCAGAATTCCAGGAAGGCA	
AE10481	TGTAAAACGACGCCAGTGTGGTCTTTAAAAGGAGGCCTG	1374	CAGGAAACAGCTATGACCGACTTTTGCACCAACCG	1495
AE104810	AE104s10 TGTAAAACGACGGCCAGTGGTCTCAGCACTGTGATCCTC	1375	CAGGAAACAGCTATGACCGTGCTACGTACATGTGA	1496

AE104s11	AE104s11 TGTAAAACGACGGCCAGTTCGGGAGTTGTAACAAATGCT	1376	CAGGAAACAGCTATGACCGAGGCTGTGTTTTGTCA	1497
AE104s12 7	TGTAAAACGACGGCCAGTGCTATGCAAAAACCTCATCCA	1377	CAGGAAACAGCTATGACCGAGGCTGTGTTTTGTCA	1498
AE104s13 7	AE104s13 TGTAAAACGACGGCCAGTCATCTACACCATGCATAGGGC	1378	CAGGAAACAGCTATGACCTGGAGGAAGAAAACAGG	1499
AE104814 7	TGTAAAACGACGCCAGTTAGCCTCTCCAGTTCTAGCCC	1379	CAGGAAACAGCTATGACCATTTCTAATCGGTCTTG	1500
AE104816 7	TGTAAAACGACGGCCAGTAATAAAAGAGGTGCTGACCCAC	1380	CAGGAAACAGCTATGACCCTAGAATCATAGGCGCA	1501
AE104s17 7	TGTAAAACGACGGCCAGTCCACCATGACCCAAGTTTAT	1381	CAGGAAACAGCTATGACCGCCACTTGTTTCATACT	1502
AE104s18 7	TGTAAAACGACGCCAGTGAGGAATCCCTTTGACTCACC	1382	CAGGAAACAGCTATGACCGACTGAGCAATGTCTGG	1503
AE104819 7	TGTAAAACGACGACCAGTTGGTTCCTTCAACTGTTGTCC	1383	CAGGAAACAGCTATGACCACAAACGTCCATTGAGT	1504
AE104s2 7	TGTAAAACGACGGCCAGTGTGGTCTTTAAAGGAGGCCTG	1384	CAGGAAACAGCTATGACCGACTTTTGCACCAACCG	1505
AE104820 7	AE104s20 TGTAAAACGACGGCCAGTAGATGTATGGCGGGAGGTTTCT	1385	CAGGAAACAGCTATGACCGCCACCCATAAACTGAT	1506
AE104s21 1	AE104s21 TGTAAAACGACGGCCAGTTTTTGGATGTAAACAGTGGGC	1386	CAGGAAACAGCTATGACCAATGTTTTGAAAGTCCC	1507
AE104s22 7	TGTAAAACGACGGCCAGTGGAAGCCCCCATGTGAATT	1387	CAGGAAACAGCTATGACCTTGAGCAAAACTGAGAA	1508
AE104s23 1	TGTAAAACGACGGCCAGTACTTCAGTCGCTCCCTGGTAC	1388	CAGGAAACAGCTATGACCACATGGAAATCTTCGCA	1509
AE104824 1	TGTAAAACGACGCCAGTTCTCCATCTGAATGGGTTCTG	1389	CAGGAAACAGCTATGACCACGAGATGCAGAAGTTC	1510
AE104s25 1	AE104s25 TGTAAAACGACGGCCAGTAAGCAACTGTCCCTCAATCCT	1390	CAGGAAACAGCTATGACCTAATCACACAGATCGCC	1511
AE104s26 1	TGTAAAACGACGACGAGTGACCTCCTTGTCCATCAGTGA	1391	CAGGAAACAGCTATGACCCCAAGGACTCCAAAATC	1512
AE104827 7	TGTAAAACGACCAGTCCCTCACAACGACTTCATGTT	1392	CAGGAAACAGCTATGACCTCACTGATGGACAAGGA	1513
AE104s28 7	TGTAAAACGACGCCAGTTTCTCTCCCAAATGCTCCTGTG	1393	CAGGAAACAGCTATGACCGGGTGATATGGACAGCA	1514
AE104s29 7	AE104s29 TGTAAAACGACGGCCAGTGGTCTCAGCACTGTGATCCTC	1394	CAGGAAACAGCTATGACCGTGCTACGTACATGTGA	1515
AE10483 1	TGTAAAACGACGGCCAGTGCAGGCAAATACCACTTTCAA	1395	CAGGAAACAGCTATGACTTGGATGAAAAGAGGA	1516
AE104830 1	TGTAAAACGACGGCCAGTCCCAATACTGATTCTGCTCCA	1396	CAGGAAACAGCTATGACCGGAACTCAAAGACTCAA	1517
AE104831 7	TGTAAAACGACGACCAGTTGGTTCCTTCAACTGTTGTCC	1397	CAGGAAACAGCTATGACTTGAGTCAGGGACTCAG	1518
AE104832 7	TGTAAAACGACGACCAGTCCTGACTCAATGGACGTTTGT	1398	CAGGAAACAGCTATGACCAATCCATATTCACACCA	1519
AE104833 1	TGTAAAACGACGCCAGTCCTGACTCAATGGACGTTTGT	1399	CAGGAAACAGCTATGACCAATCCATATTCACACCA	1520
AE104834 1	TGTAAAACGACGCCAGTATCTTCCTCTGCCTCATCACA	1400	CAGGAAACAGCTATGACCTATTGCACAACCATCTG	1521
AE104835 T	TGTAAAACGACGGCCAGTTCAGACTTTGAAGACATGGCC	1401	CAGGAAACAGCTATGACCTATTGCACAACCATCTG	1522
	TGTAAAACGACGCCAGTTGTACGTAGCACCCTTTGCTT	1402	CAGGAAACAGCTATGACCTCACTGATGGACAAGGA	1523
AE104s4 1	TGTAAAACGACGGCCAGTGAATCCCAAAGAGATTGAGGC	1403	CAGGAAACAGCTATGACCACAAGCTTGGAGGAAGC	1524
	TGTAAAACGACGGCCAGTGAATCCCAAAGAGATTGAGGC	1404	CAGGAAACAGCTATGACCGACATTCCACAGTTGTG	1525
$\neg$	TGTAAAACGACGCCAGTTGCTTCCTTTTTTCATCCAA	1405	CAGGAAACAGCTATGACCCAGCCTACAGGAAGTGG	1526
AE104s7 T	TGTAAAACGACGCCAGTGGACCCACAAATCAATGCTT	1406	CAGGAAACAGCTATGACCATACCAACAGCTTCCCC	1527
_	TGTAAAACGACGCCAGTTGCTCCACGGAGCTATTTCTA	1407	CAGGAAACAGCTATGACCCAAAGACTCAAGTGGGA	1528
$\neg$	TGTAAAACGACGCCAGTGTGGGAATGACAGGTGGAAG	1408	CAGGAAACAGCTATGACCGGGTGATATGGACAGCA	1529
$\overline{}$	TGTAAAACGACGGCCAGTAGAGCATCCTCTTTACCCCA	1409	CAGGAAACAGCTATGACCACTGTACCTGCCCGGTT	1530
$\neg$	TGTAAAACGACGACCAGTAAGCCTGGAAGCTTAGGTCTG	1410	CAGGAAACAGCTATGACCTTTGATGCGGGGTAGTG	1531
	TGTAAAACGACGGCCAGTTATTTTTCTAGGTGGGGCAGCT	1411	CAGGAAACAGCTATGACCTACCCCTCTAACTTGCA	1532
	TGTAAAACGACGGCCAGTGAACCACAGGATAGAGCCTCC	1412	CAGGAAACAGCTATGACCATCTGTTGGGAGCTGGG	1533
	TGTAAAACGACGCCAGTACTACCCAGCTCCCAACAGAT	1413	CAGGAAACAGCTATGACCTGGATTGGTGACTCTTA	1534
AE105s6 T	TGTAAAACGACGGCCAGTGGACCCAGATCTTCAGGTTTC	1414	CAGGAAACAGCTATGACCAACTGAGAGCTGAGGCT	1535
AE10681 T	TGTAAAACGACGCCAGTAGAGTGGCCAATCTTCCACTT	1415	CAGGAAACAGCTATGACCGTGGATCATCTTAGCCC	1536
AE10682 T	TOTAAAACGACGCCAGTGGCATGGGGGGGGGTCATCTTAC	1416	CAGGAAACAGCTATGACCTGGCAGGAAAATATGG	1537
AE10683 T	TGTAAAACGACGCCAGTCAGATCTGGGTTCCAAAGACA	1417	CAGGAAACAGCTATGACCCTGATCTACTTCCTCCC	1538
AE106s4 T	TGTAAAACGACGCCAGTCTTTTGTTCACCCTGTCAAGC	1418	CAGGAAACAGCTATGACCTTGCAAAAAGGGTCAGT	1539
	TGTAAAACGACGGCCAGTGGCTCCAGGAAAATGAGTCTT	1419	CAGGAAACAGCTATGACCTCTGGAACCATCAGAAA	1540
AE106s6 T	TGTAAAACGACGGCCAGTAAAAGCTGGTCCGACCTTTTA	1420	CAGGAAACAGCTATGACCTCCAACTGCTCTTCACG	1541
	TGTAAAACGACGGCCAGTTGGGGGGGTGTTTCTGATGGTTC	1421	CAGGAAACAGCTATGACCATGAAATCCACCCGGTA	1542
$\overline{}$	TGTAAAACGACGCCAGTATGGATTTCTGGTTCCCTTTG	1422	CAGGAAACAGCTATGACCCTTCTTCCTCCTGCCCT	1543
AE106s9 T	TGTAAAACGACGCCAGTCTTTAAGAGCAAGCGAAGTGG	1423	CAGGAAACAGCTATGACCCACACTATGGGCCAGTG	1544
AE107s1 T	TGTAAAACGACGCCAGTAATTGTATGTGGGGGCAGACT	1424	CAGGAAACAGCTATGACCGTGAAGCAGATGCCTGG	1545
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AE10782	AE107s2 TGTAAAACGACGGCCAGTCCTGACAGGCCTGCTGATAC	1425	CAGGAAACAGCTATGACCATTTTGAGGTCCACACA	1546
AE10783	AE107s3 TGTAAAACGACGGCCAGTGCCCAGTTTGTTCATGTCAGT	1426	CAGGAAACAGCTATGACCGGAAATGAGACTACGAA	1547
AE107s4	TGTAAAACGACGGCCAGTCCTGACAGAGCCTGCTGATAC	1427	CAGGAAACAGCTATGACCAAGTCTGTCACCTTCTG	1548
AE107s5	AE107s5 TGTAAAACGACGGCCAGTCCCTACCCCCAGTAAAATCAA	1428	CAGGAAACAGCTATGACCACCTCTCAGCCTCAGAC	1549
AE107s6	AE107s6 TGTAAAACGACGGCCAGTGCCGTCAGAGTGCTGTCTTAT	1429	CAGGAAACAGCTATGACCCTGTTTGTCTGCACCTG	1550
AE109s1	TGTAAAACGACGCCAGTTGACGAGAGTCAATTGAAAGGA	1430	CAGGAAACAGCTATGACCATGCAGACCAAAGCATC	1551
AE109s2	AE109s2   TGTAAAACGACGCCAGTCAAAGTAGTTGAGCAGTGGCC	1431	CAGGAAACAGCTATGACCGACCATACAACAATTGG	1552
AE10983	TGTAAAACGACGCCAGTAAATGGCAGCTGTCACCATAG	1432	CAGGAAACAGCTATGACCACATGAATGTAAGGCCA	1553
AE109s4	AE109s4 TGTAAAACGACGCCAGTTCTGCAGAGAAAATAAACCACTGA	1433	CAGGAAACAGCTATGACCTCTTCAGCAAAATTTCC	1554
AE10985	AE109s5 TGTAAAACGACGCCAGTGCATTCTTGTGGATTATCTGGG	1434	CAGGAAACAGCTATGACCTCGACAGTGGGGAAACT	1555
AE109s6	AE109s6 TGTAAAACGACGCCAGTTTGCCCCATAGTGGTAACTTGC	1435	CAGGAAACAGCTATGACCCGAGTGGCTAATTTGAA	1556
AE109s7	AE109s7 TGTAAAACGACGGCCAGTGCACACAGGAAGAACACACAA	1436	CAGGAAACAGCTATGACCCTCCCCCATGTCTCTCT	1557
AE10988	TGTAAAACGACGCCAGTGTGCATGCATCTGTGTGTT	1437	CAGGAAACAGCTATGACCACATGAATGTAAGGCCA	1558
AE10989	AE109s9 TGTAAAACGACGCCAGTTGCTTTCAAAATGCGATTTCT	1438	CAGGAAACAGCTATGACCCTTTCTTCCTGGGCTTT	1559
AE110s1	AE110s1 TGTAAAACGACGCCAGTCAGGCATGTCAGGTTTTGAAT	1439	CAGGAAACAGCTATGACCTTGTAATCCATCCGTAG	1560
AE110s10	AE110s10 TGTAAAACGACGGCCAGTCTTGCTGTGTTATCCCCAAGA	1440	CAGGAAACAGCTATGACCCTCCTGCTTGGAACAGA	1561
AE110s11	AE110s11 TGTAAAACGACGGCCAGTAAGAACATCTTTTTTCTCCCCG	1441	CAGGAAACAGCTATGACCATCCACAATCTTCCCTC	1562
AE110812	AE110s12 TGTAAAACGACGGCCAGTGCAGGTCATGGAAGTGGATTA	1442	CAGGAAACAGCTATGACCAGCCATTTAGTTTGACC	1563
AE110s2	AE110s2 TGTAAAACGACGGCCAGTGATCTGGAGCGACTGTTTCTG	1443	CAGGAAACAGCTATGACCTTTGCTTAGGGA	1564
AE11083	AE110s3 TGTAAAACGACGGCCAGTCTTTCAACATCCATTTGTGGG	1444	CAGGAAACAGCTATGACCTGACGACTTACTTTGGA	1565
AE110s4	AE110s4 TGTAAAACGACGCCAGTCACAGGAAGCAACCTCTGAAG	1445	CAGGAAACAGCTATGACCGGAGCCAGAAATGGAGA	1566
AE11085	AE110s5 TGTAAAACGACGCCAGTCCTTGCAAAATTCCTGAATGA	1446	CAGGAAACAGCTATGACCAGGGTTGCTCAACCCTA	1567
AE11086	AE110s6   TGTAAAACGACGCCAGTCCTTGTCTGTACGGGGTAACA	1447	CAGGAAACAGCTATGACCCCAACAGAGCAGGAAAT	1568
AE110s7	AE110s7   TGTAAAACGACGACCAGTAACGGGTACCAATTCTATCCC	1448	CAGGAAACAGCTATGACCCTAGCACATATCCCAGC 1	1569
AE110s8	AE110s8   TGTAAAACGACGACCAGTGATTTTGGGTGGATAGAAGCC	1449	CAGGAAACAGCTATGACCGGTTTACAAACCACTTT 1	1570
AE110s9	AE110s9 TGTAAAACGACGCCAGTGAAGGGTGCATGCCTGTAGT	1450	CAGGAAACAGCTATGACCTAAGTGACCTGCCCAAA	1571

Table XII Sample Description

	Cases			Controls		
Angi	Angioedema-like	Total	Angioedema	Angioedema-like	Total	Total
	10	21	32	19	51	72
	22	34	38	69	107	141
	1	-	0	-	$\vdash$	7
	33	26	70	68	159	215

Table XIII
Candidate Angioedema Susceptibility Genes

Gene ID	BDKRB2	KLK1	XPNPEP2
Gene	Bradykinin B2 Receptor	Tissue Kallikrein	Aminopeptidase P (Membrane Bound)
Chromosome	14	19	X

Association of SNPs of the present invention with Angioedema and/or Angioedema-like Events Table XIV

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:		sample or	ocores 1 est			Estimate		ot Kare	ŏ	Lower 95%		
Gene ID SNP ID	SNP ID	Subgroup		DF	Probability	Type	$A,a^1$	Allele	$(OR)^2$	ਹੋ	T T	$p(a)^3$
BDKRB2	AE104s9	3DKRB2 AE104s9 Caucasians	7.01	7	0.0300	Asymptotic	A,T	1	3.41	1.3238	8.7969	0.28
					0.0251	Exact			3.37	1.2261	10.2718	
KLK1	AE107s2	Blacks	7.50	2	0.0062	Asymptotic	C,T	1	5.64	1.4211	22.3807	0.09
					0.0062	Exact			5.64	1.2422	34.7611	
XPNPEP2	XPNPEP2 AE100s4	Caucasians	13.44	7	0.000	Exact	C,T	2	14.95	1.9838	+INF	0.28
		Angioedema-like	11.39	7	0.0022	Exact		2	10.82	1.3105	+INF	0.22
		Overall	10.72	5	0.0047	Asymptotic		7	11.11	1.2687	97.2709	0.23
1 16			,		1 11							

Most frequent (common) allele, least frequent (rare) allele.

of copies of the rare allele, relative to controls matched for nationality, race, gender and starting dose, over the odds of such The ratio of the odds of an adverse event (angioedema and/or Angioedema-like) in subjects carrying the specified number an adverse event for similarly matched subjects not carrying any copies of the rare allele.

3 Rare allele relative frequency.